

WEST Search History

DATE: Tuesday, December 31, 2002

<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
side by side			result set
<i>DB=USPT,PGPB,EPAB,DWPI,TDBD; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
L2	L1 and carrot	16	L2
L1	antifreeze adj (polypeptide? or peptide? or protein?)	98	L1

END OF SEARCH HISTORY

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 18:56:19 : Search time 1305.46 Seconds

(without alignments)
12624.425 Million cell updates/sec

Title: US-09-308-140-6

Sequence: 1 atgaattatgaatcattt.....ctccattgccgaatgctag 999

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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3: gb_in:*
4: gb_om:*
5: gb_ov:*
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36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	999	100.0	999	6	A91926
2	999	100.0	1140	8	AF053480
3	999	100.0	1238	8	AF053480
4	584.4	58.5	829	6	DCA131340
5	356.2	35.7	1285	8	AF1931
6	332	33.2	1162	8	ADPGIP
7	328.8	32.9	1057	8	MDU77041
8	328.8	32.9	1057	8	PPRPG1
9	295.4	29.6	1052	6	128276
10	290.4	29.1	2075	8	AF305093
11	290.4	29.1	2075	6	128277
12	284	28.4	909	8	AF159167
13	284	28.4	909	8	AF159170
14	284	28.4	909	8	AF159171
15	284	28.4	909	8	CSPGIP
16	283.2	28.3	984	8	AB015643
17	283.2	28.3	984	8	AB016204
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19	281.6	28.2	984	8	AB015198
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22	280	28.0	984	8	AB015356
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42	237	23.7	751	8	AF196902
43	237	23.7	751	8	AF196931
44	236.6	23.7	751	8	AF196867
45	235.4	23.6	751	8	AF196900

ALIGNMENTS

RESULT 1
LOCUS A91926
DEFINITION Sequence 6 from Patent WO9822591.
ACCESSION A91926
VERSION A91926.1 GI:6740789
KEYWORDS
SOURCE
ORGANISM
Daucus carota

REFERENCE
AUTHORS Byass, L.J. and Doucet, C.J.
TITLE CARROT ANTIFERREZE POLYPEPTIDES
JOURNAL Patent: WO.9822591-A 6 28-MAY-1998.
BYASS LOUISE JANE (GB); DOUCET CHARLOTTE JULIETTE (GB)

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BASE COUNT 277 a 266 c 185 g 271 t
ORIGIN

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Best Local Similarity 100.0%: Pred. No. 7.3e-287;
Matches 999: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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RESULT 2

AF055480 1140 bp mRNA PLN 06-OCT-1998
LOCUS Daucus carota antifreeze protein (AFP) mRNA, complete cds.
DEFINITION
ACCESSION AF055480
VERSION AF055480.1 GI:3702802
KEYWORDS
SOURCE carrot.
ORGANISM Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids II; Apiales; Apiaceae; Daucus.
1 (bases 1 to 1140)
Lillford, P., Telford, J., Holt, C. and Bowles, D.
A carrot leucine-rich repeat protein that inhibits ice
recrystallization
Science 282 (5386), 115-117 (1998)
98429644
2 (bases 1 to 1140)
Worrall, D.
Direct Submission
Submitted (23-MAR-1998) Biology, University of York, University
Road, PO Box 373, York YO1 5YW, UK
location/Qualifiers

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1. 1140
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/note="similar to plant polygalacturonase inhibitor
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BASE COUNT

332 a 284 c 208 g 316 t
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Query Match 100.0% Score 999: DB 8: Length 1140:
Best Local Similarity 100.0%: Pred. No. 7.4e-287;
Matches 999: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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RESULT 3
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LOCUS

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DEFINITION Daucus carota afp gene.
ACCESSION AJ131340
VERSION AJ131340.1 GI:4455919
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SOURCE Daucus carota
ORGANISM Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
1 (bases 1 to 1238)
Meyer K., Kell, M. and Naldrett, M. J.
A leucine-rich repeat protein of carrot that exhibits antifreeze
activity
FEBS Lett. 447 (2-3), 171-178 (1999)
99229753
REFERENCE 2 (bases 1 to 1238)
AUTHORS Meyer K.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-1998) Meyer K., Forestry Research Unit, Shell
International Renewables, HRI East Mallings, Kent ME19 6 BJ, UK
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Best Local Similarity 100.0%; Pred. No. 7,4e-287;
Matches 999; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 332 GCTTATGAGTCCGTAACCTCCCAATCTTTGCGAAATCCAGAAATTTCTGCA 391
QY 361 CTCAAGAGCTTAAATCCCTGAGCTGAGCGAGCATGCTGAGCTGCTCTTA 420
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Db 692 AGGCTCAGCTCCTCAGGAGCAAGAGTGAATATTCATTTGTTGGGCTTAA 751
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RESULT 4
LOCUS A91931 829 bp DNA PAT 22-JAN-2000
DEFINITION Sequence 11 from Patent WO9822591.
ACCESSION A91931
VERSION A91931.1 GI:6740793
KEYWORDS
SOURCE
ORGANISM Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
REFERENCE
AUTHORS Byass, L.J. and Doucet, C.J.
TITLE CARROT ANTIFREEZE POLYPEPTIDES
JOURNAL Patent: WO 9822591-A 11 28-MAY-1998;
BYASS LOUISE JANE (GB); DOUCET CHARLOTTE JULIETTE (GB)

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BASE COUNT      235 a      176 c      160 g      258 t

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Query Match          58.5%; Score 584.4; DB 6; Length 829;
Best Local Similarity 99.0%; Pred. No. 3.4e-163;
Matches 588; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 61 AACAACTTTTGGGTATATCCCTCTCAGCTTCCACCTTCCGAACTTAAAGCCCTG 120
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QY 586 tcccgagacatalatcttcgacataaccagctcaccggttctgttcccaaaactttctc 645
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Db 361 AATTCTCCAGGAGTCCAGAGTTTCCACCCTCTTGGACATATTAGACTTGAACCATTAAC 420
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RESULT 5
LOCUS ADPGIP 1285 bp mRNA PAT 28-JAN-1999
DEFINITION A. deliciosa pgip mRNA for polygalacturonase inhibitor.
ACCESSION Z49063
VERSION Z49063.1 GI:1143380
KEYWORDS polygalacturonase inhibitor.
SOURCE Actinidia deliciosa.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Query Match	Best Local Similarity	Score	32.9%	328.8	DB: 8	Length	1057
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DEFINITION	Sequence 1 from patent US 5569830.		PAT
ACCESSION	I28276		
VERSION	I28276.1	GI:1819052	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1058)		
TITLE	Bennett, A., Labavitch, J. M., Powell, A. and Stoltz, H.		
JOURNAL	Plant inhibitors of fungal polygalacturonases and their use to		
FEATURES	control fungal disease		
SOURCE	Patent: US 5569830-A 1 29-OCT-1996;		
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RESULT 13
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DEFINITION Eucalyptus saligna polygalacturonase-inhibiting protein (pgip)
ACCESSION AF159170
VERSION AF159170.1 GI:6651281
KEYWORDS
SOURCE ORGANISM
Eucalyptus saligna.
Eucalyptus saligna
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids II; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 909)
Chimamurombe, P.M., Botha, A.M., Wingfield, M.J. and Wingfield, B.D.
Molecular relatedness of the polygalacturonase-inhibiting protein
genes in Eucalyptus species
Theor. Appl. Genet. 102, 645-650 (2001)
2 (bases 1 to 909)
Chimamurombe, P.M., Oberholster, A., Wingfield, M.J. and
Wingfield, B.D.
Direct Submission.
Submitted (15-JUN-1999) Genetics, Faculty of Agricultural and
Biological Sciences, University of Pretoria, Forestry and
Agricultural Biotechnology Institute, Pretoria 0001, South Africa
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Db 421 GCTCCGAACCTCAAGCGCTCTTATAGACCCCAATTAAGCTCAAGGTCATATTCGGA 480
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta: eudicotyledons: core eudicots;
Rosidae: eucosids II; Sapindales: Rutaceae: Citrus.

REFERENCE 1 (bases 1 to 1207)
AUTHORS Mayer, R.T.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1207)
AUTHORS Mayer, R.T.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-1996) R.T. Mayer, USDA, ARS, HRS, Subtropical
Plant Insect Research Unit, 2120 Camden Road, Orlando, Florida,
32803, USA

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ORIGIN

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Best Local Similarity 59.4%; Pred. No. 1.5e-73;
Matches 558; Conservative 0; Mismatches 370; Indels 12; Gaps 4;

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GenCore version 4.5
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Searched: 930621 seqs, 428662619 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	250.8	25.1	1164	21	AAC33759
6	249.2	24.9	1157	21	AAC48837
7	218	21.8	1175	21	AAC39926
8	194.8	19.5	1079	21	AAC36540
9	181	18.1	1518	21	AAC54534
10	177.6	17.8	1528	21	AAC52792
11	172.4	17.3	1117	14	AAO42595

12	170.8	17.1	2917	18	AAT86755	Raspberry drui gen
13	138.8	13.9	792	14	AAO42596	Sequence of varian
14	97.6	9.8	1400	22	AAO1017	Maize disease resi
15	75.6	7.6	3341	19	AAV14522	CF-5 pathogen resi
16	71.8	7.2	3979	19	AAV14518	CF-5 pathogen resi
17	71.8	7.2	3979	19	AAV14519	CF-5 pathogen resi
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21	62.6	6.3	3396	18	AAV79268	Pinus radiata cell
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23	59.6	5.9	1052	21	AAV79691	Pinus radiata cell
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ALIGNMENTS

RESULT 1

ID AAT49434 standard; CDNA; 1058 BP.

AC AAT49434;

DT 05-MAR-1997 (first entry)

DE Pear polygalacturonase inhibitor protein CDNA.

XX PCIP: polygalacturonase inhibitor protein; fungal resistance;

KM Botrytis cinerea; transgenic plant; tomato; strawberry; ss.

XX Pyrus communis cv. Bartlett.

OS Key Location/Qualifiers

FT CDS 34..1026

FT /tag= a

FT /product= polygalacturonase_inhibitor

PN US5569830-A.

XX 29-OCT-1996.

PF 03-MAY-1994; 94US-0238163.

PR 03-MAY-1994; 94US-0238163.

XX (REGC) UNIV CALIFORNIA.

PI Bennett A, Labavitch JM, Powell A, Stoltz H;

DR WPI, 1996-496968/49.

DR P-PSDB: AAM09095.

Hand done

XX DNA construct, comprising polygalacturonase inhibitor protein DNA
 PT - useful to confer resistance to fungal, partic. Botrytis cinerea,
 PT infection in plant, pref. tomato or strawberry
 XX
 PS Claim 2; Fig 1; 33pp; English.

CC The pear polygalacturonase inhibitor protein cDNA was obtained using
 CC mRNA isolated from mature green fruit. Pear PGIP exhibits differential
 CC inhibition of polygalacturonases from different fungal species:
 CC introduction of the pear PGIP cDNA into other plant species alters the
 CC susceptibility of these plants to the fungal pathogens against which
 CC pear PGIP is effective. For example, transgenic tomato fruit
 CC expressing high levels of pear PGIP were shown to be more resistant
 CC to the fungus Botrytis cinerea than control fruit.

XX Sequence 1058 BP: 268 A; 340 C; 198 G; 252 T; 0 other;

Query Match 32.9%; Score 328.8; DB 17; Length 1058;
 Best Local Similarity 60.2%; Pred. No. 1.7e-96;
 Matches 600; Conservative 0; Mismatches 387; Indels 9; Gaps 3;

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 OY 187 gacctagtgaaatgtgcgaaccgaaccgaatcttccctcaatcaagacgac 246
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RESULT 2

AAT49435 standard; DNA: 2075 BP.

XX AAT49435;
 XX
 DT 05-MAR-1997 (first entry)

DE Tomato polygalacturonase inhibitor protein genomic DNA.

XX PGIP; polygalacturonase inhibitor protein; fungal resistance;

KW Botrytis cinerea; transgenic plant; tomato; strawberry; ss.

XX Lycopersicon esculentum.

XX Key Location/Qualifiers

FT CDS 421..1404

FT /tag= a

FT /product= polygalacturonase_inhibitor

FT 1545..1550

FT /tag= b

XX US5569830-A.

XX 29-OCT-1996.

XX 03-MAY-1994; 94US-0238163.

XX 03-MAY-1994; 94US-0238163.

XX (REGC) UNIV CALIFORNIA.

XX Bennett A, Labavitch JM, Powell A, Stoltz H;

XX WPI: 1996-496968/49.

XX P-PSDB: AAM09096.

PT DNA construct, comprising polygalacturonase inhibitor protein DNA
 PT useful to confer resistance to fungal, partic. Botrytis cinerea,
 PT infection in plant, pref. tomato or strawberry

PS Claim 4; Fig 2; 33pp; English.

CC A fragment of tomato genomic DNA without introns and coding for
 CC the polygalacturonase inhibitor protein was isolated from mature
 CC green fruit. The DNA coding for PGIP can be introduced into other
 CC plant species, e.g. strawberry, to alter the susceptibility of
 CC these plants to the fungal pathogens against which tomato PGIP is
 CC effective.

XX Sequence 2075 BP: 660 A; 366 C; 348 G; 701 T; 0 other;

Query Match 29.1%; Score 290.4; DB 17; Length 2075;

Best Local Similarity 58.6%; Pred. No. 7.5e-84;
Matches 564; Conservative 0; Mismatches 386; Indels 12; Gaps 3;

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ID AAC48852 standard; DNA; 1122 BP.
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AC AAC48852;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 59011.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
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PR 29-OCT-1999; 99US-0162142.

Query Match 25.7%; Score 256.8; DB 21; Length 1122;
Best Local Similarity 56.0%; Pred. No. 4; 6e-73;
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Db 664 taggaacaatcgaacttaacccgactgaattatccgcacagaagctccaagtgatgctt 723
Oy 701 catctctgttggcctaaacgcttggaaatgctgaatttccagaacgctgctta 760
Db 724 cgatctgttcttggtcccaacaaacacctgctcatatgaacttaagaacatgcttc 783
Oy 761 gttcaatttctccagggtycagagattccaccctcttgcacataacttagactgaacc 820
Db 784 agtgcataatcccaaggt--tgatattcccaacaaacttgatcttgactgaacc 840
Oy 821 ataaccagaatcgaggaagctgctgagtgaaatggtcaattggaactgcagacattta 880
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Oy 941 accgtaggcctatctccacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 999
Db 961 attctattcctatttccacaaacagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1019

RESULT 5

AAC33759 AAC33759 standard; DNA; 1164 BP.

AAC33759;

17-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 4212.

Hybridisation assay: genetic mapping; gene expression control;

protein identification; signal transduction pathway;

metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

23-MAR-1999; 99US-0125788.

25-MAR-1999; 99US-0126264.

29-MAR-1999; 99US-0126785.

01-APR-1999; 99US-0127462.

06-APR-1999; 99US-0128234.

08-APR-1999; 99US-0128714.

16-APR-1999; 99US-0129845.

19-APR-1999; 99US-0130077.

21-APR-1999; 99US-0130449.

23-APR-1999; 99US-0130510.

28-APR-1999; 99US-0130891.

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RESULT 6
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XX
AC AAC48837;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58956.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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Db 1000 ttcctagtcgcaag 1013

RESULT 7

AC AAC39926 standard; DNA; 1175 BP.

AC AAC39926;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 26411.

DE Arabidopsis thaliana.

KW Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EPI03405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

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Query Match 21.8%; Score 218; DB 21; Length 1175;
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 ID AAC36540:
 AC AAC36540:
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 DT 17-OCT-2000 (first entry)
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 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14181.
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 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 OS Arabidopsis thaliana.
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PN EPI033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000. 2000EP-0301439.
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Query Match 19.5%; Score 194.8; DB 21; Length 1079;
 Best Local Similarity 55.4%; Pred. No. 6.5e-53;

Matches 420; Conservative 0; Mismatches 332; Indels 6; Gaps 2;

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OY 92 acaagacaagaagcttacttcaaatcaaaacagccttgaaaacccacattacag 151
DB 107 aagatgacaataactacccctcctcaagaatacctaataaacaccttaccacctcg 166
OY 152 actcatgggtctcagacagcatgttgggttggacctagtcgaatgtgacgaaca 211
DB 167 cctcatggatcccaaaaacagcactgttctgtctgttacttgcctcgagtcgagcgacta 226
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RESULT 9
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XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 78205.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
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DB 1303 GTAAACCAAAATACAAAACACCTCTCAGATCAGAAATCTTAACAAACCTTATC 1244
OY 146 ttacagactcaggtgtgtcagacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 205
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DB 1183 ACGCCACCCCTTAACCCAGCTTACCGCTTAACCATATTCCTCCGCGAGATCTCCGGTC 1124
OY 263 aaatcccaactaaggt 322
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DB 1063 CTAACCTCAACCGGTACATCCAAACCCACCATGCGCAACTCAAGAACTCGCAATGCTCA 1004
OY 383 gactcagctcagcagctcagctcagctcagctcagctcagctcagctcagctcagctc 442
DB 1003 GCGTACGCTGAGCAATGTGACAGGTCTGCAATCTGCAATCTTAAGTACGCTCAAGCAATC 944
OY 443 taactgttgaactcagctcagctcagctcagctcagctcagctcagctcagctcagctc 502
DB 943 TCGAGTCTTGAACCTTCTTCAATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884
OY 503 ctcttcggaactaaagccctcagctcagctcagctcagctcagctcagctcagctcagctc 555
DB 883 CGTTACCTAAATCTGGCTCTTGAAGCTTAGCAGAACAACTTACAGTAAGAAGCAT 824
OY 556 ----- 555
DB 823 CTTTCTTTATATACATCATTCAGTCTTGTCTTAACACGATCTTATGTTAGGTT 764
OY 556 --atcccgatactcttgggaatttgcgtgac---cccgacataatacttgcata 610
DB 763 CCAATCCAGAGTCATTTGGTGTGCTTCCAGGAACGCTCCGACCTTGGCTATACATA 704
OY 611 accaactcagcaggtgtgtcctcaaaacttgcctagagcagatcaaatgtgcctcagct 670
DB 703 ACGACTCTCCGGTCCATACCAAAATATTAGCAACATGACTTAAACCGAGATCGATT 644
OY 671 tctcaggaacagactagaaggtgatactcattctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 730
DB 643 TATCCCGCAACAGCTCCAGAGTGTGATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 584
OY 731 aaatgtcagatcttccaggaagcgt 790
DB 583 GGTCTATTGACTTATCAAGAAACAGTTCAGTTCGATATCTCAAGGT---TGATATCC 527
OY 791 caacctcttgaacatactagaactgaacacaaacacagcagcagcagcagcagcagcagcagc 850
DB 526 CTAACAACTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 467

OY 851 aatgtcctaattgtgactctgcagacattaacgttcagatgataataatcttcgcgcaaga 910
DB 466 AGTGACTGAAGCTCTCTCTTCAATGTTAGCTACAACTGTGTGACACA 407
OY 911 ttccacaggggaacactccagagatccagccgtaacccatctccacacagctgtct 970
DB 406 TCCCACTGAGAGGAAATTCAGACATTTGATTTCTTATCTCTATTTTCACAAAGTGT 347
OY 971 tgt 999
DB 346 TGT 318

RESULT 10
AAC52792/c
ID AAC52792 standard; DNA: 1528 BP.
XX
AC AAC52792:
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 72454.
XX
KW Hybridisation assay: generic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999: 99US-0121825.
PR 05-MAR-1999: 99US-0123180.
PR 09-MAR-1999: 99US-0123548.
PR 23-MAR-1999: 99US-0125788.
PR 25-MAR-1999: 99US-0126264.
PR 29-MAR-1999: 99US-0126785.
PR 01-APR-1999: 99US-0127462.
PR 06-APR-1999: 99US-0128234.
PR 08-APR-1999: 99US-0128714.
PR 16-APR-1999: 99US-0129845.
PR 19-APR-1999: 99US-0130077.
PR 21-APR-1999: 99US-0130449.
PR 23-APR-1999: 99US-0130510.
PR 23-APR-1999: 99US-0130891.
PR 28-APR-1999: 99US-0131449.
PR 30-APR-1999: 99US-0132048.
PR 30-APR-1999: 99US-0132407.
PR 04-MAY-1999: 99US-0132484.
PR 05-MAY-1999: 99US-0132485.
PR 06-MAY-1999: 99US-0132486.
PR 06-MAY-1999: 99US-0132487.
PR 06-MAY-1999: 99US-0132487.
PR 07-MAY-1999: 99US-0132487.
PR 11-MAY-1999: 99US-0134256.
PR 14-MAY-1999: 99US-0134218.
PR 14-MAY-1999: 99US-0134219.
PR 14-MAY-1999: 99US-0134221.
PR 14-MAY-1999: 99US-0134370.
PR 18-MAY-1999: 99US-0134768.
PR 19-MAY-1999: 99US-0134941.
PR 20-MAY-1999: 99US-0135124.
PR 21-MAY-1999: 99US-0135353.
PR 24-MAY-1999: 99US-0135629.
PR 25-MAY-1999: 99US-0136021.
PR 27-MAY-1999: 99US-0136392.
PR 28-MAY-1999: 99US-0136782.
PR 01-JUN-1999: 99US-0137222.
PR 03-JUN-1999: 99US-0137502.
PR 04-JUN-1999: 99US-0137502.

OY	47	tttccctcgtccctcgaacactctctgcatccaaaagtgcgaacacaaagcaagcaag	106
Db	1344	tgtttacatttctcaccgacctgtttgtcttAAAATCTTGTAACCAAAATGTACAATAA	12855
OY	107	cttctacccaatacaaaaagcccttgaaaaccaccactaacagactgaatggtgtcag	166
Db	1284	ccctcctacacatcacaagaattctCTTAACAACCCCTTATCACTCGCTTCATGGAACCTC	12255
OY	167	acgaagatgtctgtgtgttggtgacctagtcgaatgtgacgaaccagc---acgcgataa	223
Db	1224	AAACCGACTGTGTCTCTCGTACTGGCTTGAGTGGCGGCAACCCACCCGTTAAACACGCTG	11655
OY	224	tttccccaataatcagaagcaagcaagcctcgaacggccaatcccaactcaagtggtggag	283
Db	1154	TTACCGCCTTAAACATATTCTCCGGCCAGATCTCCGGTACGATCCCGGCTGAAGTGGTG	11055
OY	284	acctaccatacctcacaagccttattgtctcgtlaaactccccaactcttttcggaaaaatcc	343
Db	1104	ACTTGCCGATCTTCTGAAGACCCCTGTCTCGCAAACTCTTAACCTCAACCGGTACAACTC	10455
OY	344	cagaagaattctgcacctaagaagaccttaaatccctcgaactgaagctgcgacagctcca	403
Db	1044	AACCCAACCATGCGCAAACTCAAAACCTCCGATGCTCAGGCTCAGCTGAGCAATCTGA	985
OY	404	gtggacgcgtccctcttactctccccaagcttgaagaaactgaactgtttttagactatcgt	463
Db	984	CAGGTCGAATTCCTGACTTTTAAGTCAGTCAAGAAATGTGAGTTCTTAGAATCTTCT	925
OY	464	ttacaacatttgggtgttaatccctccctcgaacttccactctccgaaccttaagacc	523
Db	924	TCAAATGATCTCTCTGGTTCCATTCACAAGTTCCTCTCTACGTTACTTAAATCTTGGCTC	865
OY	524	tgcaacttagaagcaagcaactcaccgggaa-----atcccagatacttttggaa	555
Db	864	TTGAACTTAGCAGGAACAACCTTACAGGTAAGAACAGATCTTTCTTATTACATCATTT	805
OY	556	-----atcccagatacttttggaa	574
Db	804	CAGTGTCTGTCTAAACAMCAGATCTTATTGTGTAGGTTCCATACCAAGATCATTTGGGT	745
OY	575	atttgtctgatac---ccggataatactcttgcgataaccagctcaccgggtttgttc	631
Db	744	CGTTTCACAGGAACAAGTCCCTGACCTTCGGCTATTCACATTAACCAAGCTTCGCGTCCAATAC	685
OY	632	ccaaacatttctgcagagcagatccaatcttagctcgactctcgaagaaacagactagaag	691
Db	684	CCAATCATTTAGGCAACATGTGACTTTAAACCGGATGATTTATCCCGCAACAAGCTCCAG	625
OY	692	gtgataatcattcttgcttgggtcctaaaaagcttggaaatgctagatctttcagaa	751
Db	624	GTGATGCTTGATGATGTTGTTGGTTCCAAACAAAACAACCTGTGCTATTGACTATTACAGAA	565
OY	752	acgagcttagttccaattctccaggggtgcagagtttcccaaccctcttgcatcatag	811
Db	564	ACAATGTTCCAGTTTCGATATCTCAAAAGT---TGAATATCCCTTAAACACTTGTGATCTTGG	508
OY	812	acttgaaccaataccagatcagcgaagtcgtcgaatgaaatgtgtcctaatttgcagctgc	871
Db	507	ACTTGAACCAACAATGGGATCAGTGGGAATAATTCCGTCAGTGGACTGAACCTCTCTTC	448
OY	872	agacatttaacgtcagatgaataaactctctgggaagaatccaaaggggaaactcgc	931
Db	387	AGACATTTGATTTCTTATTCCTATTTCATACCAACAAGTGTGHTGHTGCTCTCTTGAA	328
OY	932	agagatcgaccgctlaagcctatctccacaagaagttgtcttgtgtgttccatctgcag	991
Db	992	aatgtcag 999	
Db	327	TTTGCAAG 320	


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Db      1796  ggcgaataccggaattctctgtcacagatacaaacctcgtcacccctcgaacttccctaca 1855
Oy      467  acaaaacttgggtgtcaatccctccacagcttccactcttccgaaccttaaacgctcgc 526
Db      1856  agcgccctccgcgaacccctccctccatctctctctcccaacctggagatca 1915
Oy      527  acttaagaatgaagaacacccgctgaatcccgatctatcttggaaatttgc---tg 583
Db      1916  catcgcagcaacacgcaatctccgcgcacatcccgacactccacgcctcgtttcgaagc 1975
Oy      584  gatcccggaacataatcttctgcataacacgacacgggttcttcccaaaacttgc 643
Db      1976  tgtttacggcgagacacatctccgcacacgcgcctcacgggaagatccaacgacttgc 2035
Oy      644  ctgagacgagatccaattagctcactctcaggaacacgacactagaaggtgatattcat 703
Db      2036  cgaatctgaacctgagcgtctcgttgaactgtctcgaacatgtcgagaggttgaacgctgcg 2095
Oy      704  tcttcttgggacctaaacacgcttgaatgtctagaatttccagaacacgttgcatt 763
Db      2096  tgtgttcgggtcagataagaacacgaagaagatatactgtgcgaagaactctctgtctt 2155
Oy      764  tcaatttccacagggcgacgaagattccacccctcttgacataacttagacttgaaccata 823
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Oy      941  acgcttcggcgctatcccaacaacagttgcttctgtgtctcattcgaagaatgc 996
Db      2333  acgttctctctatagccacaacaacagttgtgtgtctctctctctctcctcctcgcgc 2388

RESULT 13
AA042596
ID      AA042596 standard: cDNA to mRNA: 792 BP.
XX
AC      AA042596:
XX
DT      01-OCT-1993 (first entry)
XX
DE      Sequence of variant of fungine endopolylacturonase inhibitor (PGIP).
XX
KW      Fungine endopolylacturonase inhibitor (PGIP); PCR; primer:
KW      pesticide; ss.
XX
OS      Phaseolus vulgaris, strain Pintr.
XX
FH      Key
FT      Location/Qualifiers
FT      CDS
FT      2..685
FT      /*tag= a
XX
XX
XX      WO9311241-A.
XX
XX      10-JUN-1993.
XX
XX      04-DEC-1992; 92WO-IT00158.
XX
XX      06-DEC-1991; 91IT-OR00915.
XX
XX      (CNR) CONSIGLIO NA2 DELLE RICERCHE.
XX      (UIGE-) UNIV GEORGIA RES FOUND INC.
XX
XX      Albersheim P, Bergmann C, Cervone F, Darvill A;
XX      De Lorenzo G, Salvi G;
XX

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DR      WPI: 1993-197059/24.
DR      P-PSDB: AAR37818.
XX
XX      Nucleotide sequence contained in recombinant vector - encodes
PT      endo-polygalacturonase inhibitor (PGIP), useful for conferring
PT      e.g. fungal resistance to plants
XX
XX      Claim 6; page 21; 36pp; English.
XX
XX      The PGIP is capable of inhibiting activity of the fungine
CC      endo-alpha-1,4-D-poly-galacturonase enzyme (PG). PGIP is useful
CC      in plant transformation to confer fungal resistance or resistance
CC      to microorganisms pathogenicity.
XX
XX      Sequence 792 BP; 206 A; 227 C; 153 G; 206 T; 0 other;
XX
XX
Query Match      13.9%; Score 138.8; DB 14: Length 792;
Best Local Similarity 53.4%; Pred: No. 8; 9e-35;
Matches 362; Conservative 0; Mismatches 307; Indels 9; Gaps 3;

Oy      325  aatctcttcggaaataatcccgagaagaatctctgcactcaacgaactaaatccctcaga 384
Db      5  aacctcgtcgtcccaatcccccgcgcacatcgttaacttaaccacactcactatctcat 64
Oy      385  ctcaagctcgcagctcagtgccctgtcccttattcttccctcagcttaacgaacta 444
Db      65  atcacccacacacatgtctccgcgcgaataaccgatttcttctcagaatccaacccctc 124
Oy      445  acttctttagacttctcgttttaacaaacttgggtgtgaatccctccctcagtttccact 504
Db      125  gtaacctcgaacttccctcaacaacgcccctccgcgacccctccctccctcctctct 184
Oy      505  ctccgaaccttaaaagccctgcacttagaagctaaacgaactacccggttgaatcccgat 564
Db      185  ctcccaacactcgtatgaatcaatctcgaacgcaacacgacatctccgcgcacatcccgac 244
Oy      565  atcttgggaatttgc---tgatcccccgaacatataatcttgcataacacgactaac 621
Db      245  tcttaagctcatttcttgaaagctgttcacgttcgaatccatctccgaacacgctctcac 304
Oy      622  gggatttcccaaaacttcttgtagagagatccaatlaaggctcgaactccagggagac 681
Db      305  gggaaagattccgcgcgacgttgcgaatctgaacctggtcgttgcactgtctcgaaac 364
Oy      682  aactagaagtgatattcattctgttcttggtgacctaaacacgcttggaaattgtagat 741
Db      365  atgcgcaggggtgaacgctggtgtgttctcgatcagataaagaacacgacagagatacat 424
Oy      742  tttaagaacggtgcttaagttcaattctccagggtgacagagattccacacctcttg 801
Db      425  ctggagaagaactcctctgttcttgaatttgagaaggtggtgtgt---caagaacttg 481
Oy      802  acatacttagacttgaacataacgaactcagcgaagctgtgtcagtgagtgactcaaa 860
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Db      542  cttaagattctgcacagtttaattgtgtgcctcaacaactcgtgtgaggttccctcaa 601
Oy      919  gggggaaacctccagagatctgcacgctacgctatctccacaacagttgctgtgtgt 978
Db      602  ggtggaaacttgcacaacatttcaagttctcgtcttaagtcacaacaacagttgtgtgt 661
Oy      979  gctccattgcagaatgc 996
Db      662  tctcctctctcgtcctgc 679

RESULT 14
AAS01017
ID      AAS01017 standard: cDNA: 1400 BP.

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XX	AA001017;
AC	18-MAY-2001 (first entry)
XX	
XX	Maize disease resistance enhancing protein ZmLR2-1 cDNA.
DE	
KW	Maize; plant disease resistance; crop; soybean; sunflower; sorghum;
KW	carolina; wheat; alfalfa; cotton; rice; barley; millet; plant cell death;
KW	herbicide resistance; ZmLR2-1; polygalacturonase inhibiting protein;
KW	PGIP; ss.
XX	
OS	Zea mays.
XX	
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FT	5'UTR
FT	Location/Qualifiers
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FT	CDS
FT	50..1045
FT	/*tag= b
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FT	3'UTR
FT	1046..1368
FT	/*tag= c
FT	polyA_site
FT	1369
FT	/*tag= d
XX	
PN	MO200118061-A2.
XX	
PD	15-MAR-2001.
XX	
PF	06-SEP-2000; 2000MO-US24403.
XX	
PR	09-SEP-1999; 99US-0152988.
XX	
PA	(PION-) PIONEER HI-BRED INT INC.
XX	
PI	Simmons CR;
XX	
DR	WPI: 2001-226742/23.
XX	
DR	P-PSDB; AAU00447.
XX	
PT	Novel isolated maize disease resistance polynucleotide useful for
PT	increasing resistance in a plant to disease, controlling cell death,
PT	and conferring resistance to herbicides
XX	
PS	Claim 1; Page 77-79; 90pp; English.
XX	
XX	The present sequence encoding for maize ZmLR2-1 protein is 1 of 7
XX	novel disease resistance proteins (AAU00443-AAU00449). The ZmLR2-1
CC	is a leucine-rich repeat (LRR) containing polypeptide related to PIP
CC	(polygalacturonase inhibiting protein). These novel maize disease
CC	resistance polynucleotides and polypeptides are useful for enhancing
CC	disease resistance in crops and transgenic plants including maize,
CC	soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice,
CC	barley or millet. The level of disease resistance protein is increased
CC	by transforming a plant cell with a recombinant expression cassette
CC	which comprises the disease resistance polynucleotide operably linked to
CC	a promoter, or by culturing the plant cell under plant growing conditions
CC	to produce a regenerated plant, or by inducing expression of the
CC	polynucleotide to modulate the disease resistance protein in a plant.
CC	The polynucleotides encoding the disease resistance proteins are useful
CC	for increasing resistance in a plant to disease, controlling cell death,
CC	and conferring resistance to herbicides. They are useful as probes or
CC	amplification primers in the detection, quantification, or isolation
CC	of gene transcripts. They can be used for recombinant expression of
CC	the encoded polypeptides, as immunogens in the preparation and/or
CC	screening of antibodies, and in sense or antisense suppression of the
CC	polynucleotide in a host cell, tissue or plant.
XX	
XX	Sequence 1400 BP: 263 A; 486 C; 406 G; 245 T; 0 other;

[illegible]

OTHER INFORMATION: /standard_name="Pear PGIP cDNA"
S-08-238-163-1

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OY	404	gtggccctgctcccttactctccctcagcttaccgaactactgtctttagactatcgt	463
Db	803	CAGGTCGGATCCCTGAATTCCTCTTAGTCAGCTGAAGAATTGAGCTTGCCTCGATTGAAT	862
OY	464	ttacaactctttgggtgtataccctctcagcttcccaactctccgaacttaagccc	523
Db	863	ACAATCAATTTATCCGGAACAATCCCTCTTCCCTCTCTCAGCTTCCGAATTTGTCAGCA	922
OY	524	tgcacttagaagcgttaagaactcaccggttgaatcccgatatactttggaaatttcgcg	583
Db	923	TGTACTTATGATCGTAACAACCTCACCGGAACAATACCGGAATCTGTTTGGGAATTTAAAG	982
OY	584	gatcc-----ccggacatactcttcgataaccagctcaccggttgtgttcccaaa	637
Db	983	GACCAAAATATACCGATCTCTACTCTTTCACACAAAGCTTGACCGGACATGTGCCGCAT	1042
OY	638	ctttgttagagcagatcccaattaggctcgcacttccagggaaacagactagaagtgata	697
Db	1043	CTTTAGCTGATTTGAATTTTTCACGCTCTGATTTCTCCAGGAATAAGCTTGAAGAGAGATG	1102
OY	698	tttcatctctgttgggcccataaaacgcgttgaatgtcagatcttccagaanaacgtgc	757
Db	1103	TTTGCTTTTGTTCGGGAACAATAAAGACGAGTCAAGTAATGATTTATGAGGAATTTAT	1162
OY	758	ttagcttcaattctccagggtgcaggagttccaccctcttgacatacttagacttga	817
Db	1163	TGGAGTTTGGATTTTC---GAAATCCGAGTTTCTGAGAGCTTGATATCATTTGGATTTGA	1219
OY	818	accataaccgatacagggaagctctgtcgaagtaattgtcctaatttgcaccgcagaat	877
Db	1220	ATCATTAATCAAAATTTTGTGAGCTTACCAACAGAGATTGAAGATGTACCATTTGACGTTT	1279
OY	878	tcaacgcacgtgataataatctctgcgcaagatcccaacagggaagaaacctcagaat	937
Db	1280	TCATGTGAGCTTAAATATAGACTTTGTGGACAGTTTCCAAAGTGTGAAGCTTGCAGACT	1339
OY	938	tgcagcgtacgcgcctatctccacaacagttgctgtgtgtgtgtcccatctgcagaatgct	997
Db	1340	TTGATATTTACTCTTATTTTGCATACAAATGCTTTGTGGCTCTCCCTTCGGAATGTA	1399
OY	998	ag 999	
Db	1400	AG 1401	

RESULT 3

US-08-244-646-14

Sequence 14, Application US/08244646

Patent No. 5744692

GENERAL INFORMATION:

APPLICANT: Cervone, Felice

APPLICANT: De Lorenzo, Giulia

APPLICANT: Salvi, Giovanni

APPLICANT: Albersheim, Peter

APPLICANT: Darvill, Alan

APPLICANT: Bergmann, Carl

TITLE OF INVENTION: Nucleotide Sequences Coding An

TITLE OF INVENTION: Endopolylacturonase Inhibitor

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sally A. Sullivan

STREET: 5370 Manhattan Circle Suite 201

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

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1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patentin Release #1.0, Version #1.25
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/08/244,646
6  FILING DATE: 06-JUN-1994
7  CLASSIFICATION: 435
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: IT RM 91A 000915
10 FILING DATE: 06-DEC-1991
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: WO PCT/IT/00158
13 FILING DATE: 04-DEC-1992
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Sullivan, Sally A.
16 REGISTRATION NUMBER: 32,064
17 REFERENCE/DOCKET NUMBER: 19-94
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (303)499-8080
20 TELEFAX: (303)499-8089
21 INFORMATION FOR SEQ ID NO: 14:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 1116 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: double
26 TOPOLOGY: linear
27 MOLECULE TYPE: DNA (genomic)
28 HYPOTHETICAL: NO
29 ANTI-SENSE: NO
30 ORIGINAL SOURCE:
31 ORGANISM: Phaseolus vulgaris
32 STRAIN: Saxa
33 IMMEDIATE SOURCE:
34 CLONE: lambda PGIP-3.3
35 FEATURE:
36 NAME/KEY: CDS
37 LOCATION: 1..1026
38 NAME/KEY: 3'UTR
39 LOCATION: 1027..1116
40 US-08-244-646-14
41
42 Query Match 17.3% Score 172.4; DB 1: Length 1116;
43 Best Local Similarity 51.8%; Pred. No. 1.2e-45;
44 Matches 526; Conservative 0; Mismatches 466; Indels 24; Gaps 5;
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46 QY 2 tgaatatgaatcattcttcggccatttttgatatagcagtatttcctcgtccttc 61
47 Db 11 TCAATATCCCAATACCAATGCTTCTTAAGCTTAAGCATATTTTGGTCAATCTTGATCTT 70
48
49 QY 62 caaacctctctgcatacaaaagatgcaacaacaacaagcaagcattactccaatca 121
50 Db 71 TGAGACATGCACTCTCAAGAGTATGCAACCAACAAGATTAAGCAAGCCCTTCACAAATCA 130
51
52 QY 122 aaacagccttgaaaaaaccccccaattacagactcatgggtgtgcagaacagctgttgy 181
53 Db 131 AGAAGAGACTTGGCAACCAACCACTCTCTCTTCATGGCTTCCAACCAACCGACTGTGTA 190
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55 QY 182 gtctggac-----tagtcgaatgtgcaaacacgaacgcaactaaattccctcaatlc 238
56 Db 191 ACAAGACTGGCTAGGTTTATTATGCGACACCGACACCAACCAATATGGCTCACAMACC 250
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61 QY 287 tacatcatcctcacaagccttaagtctcgttaaacctcccaactctttcgaaaataatccag 346
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63
64 QY 347 aagaattctgcactcaaaagacctaaatccctcagaactcagctcagaacgtcagtg 406
65 Db 347 aagaattctgcactcaaaagacctaaatccctcagaactcagctcagaacgtcagtg 406

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Db 371 CCGCCATCCCTAACTACACCACTCATATCTATATCTACTACACCAATGTCGC 430
Oy 407 gccctgcccttatctatctccctcaactcagaacttaacttgtagactatcgltta 466
Db 431 GGGCAATACCGGATTTCTTGTGCACATCAAAACCTGTCACACCTGCACTTCTCTACA 490
Oy 467 acaaaccttgggtgtaacccctcctcagcttccacttccagacttaagccctgc 526
Db 491 ACGCCCTCTCCGGCACCCCTCCCTCCATCTCTCTCCCAACCTCGAGGAATCA 550
Oy 527 acttgaagcgttaagcagaccacccggtgaatcccgatctcttgggaatttgc---tg 583
Db 551 CATTGACGCGAACCGAATCTCGGCGCCATCCCGACTCTACGGCTGTTTTCGAAC 610
Oy 584 gatcccgacacatalatcttcgcataaccagctccaggttcttcccaaaacttgc 643
Db 611 TGTATTACGGGATGACATCTCCCGCACCGCTCACGGGAAGATTCCACGACGTTTG 670
Oy 644 ctgagcagatcccaattagtgctcagctctcagggagaagactagaagtgatattcat 703
Db 671 CCAATCTGAACCTGGCGTTCTGTGACTTGTCTCGAACAATGCTGGAGGCTGCG 730
Oy 704 tcttgcttggtcctaaaaacgcttggaaatgctgatttctcaggaacggtgtagt 763
Db 731 TGTGTTTCGGGTGATGAAGAACAACAGAAATACATCTGGCGAAGAACTCTTGT 790
Oy 764 tcaattctccaggggtgcaggttccaccctcttgcataactatagacttgaacata 823
Db 791 TTGATTTGGGGAAAGT---GGGGTTCTCAAGAACTTGAACGGGTGGATCTGAGGAACA 847
Oy 824 accagacacggaagctctgcagtgtaattggtctaa---attggaactcagacatla 880
Db 848 ACGGTATCTATACAGCGTACCTCAGGAGACTTAACGACGCTAAAGTTTGTGAAAGTTTAA 907
Oy 881 agctcagatataatctctcgcggaagattccaacaggggaaccccccagagattcg 940
Db 908 ATGTGACTTCAACATCTGTGGGAGATTCCTCAAGCTGGGAAGCTTGAAGAAAGTTTG 967
Oy 941 accgtacgcctatctccacacacagttgcttgggtgctccatgcccagaatgc 996
Db 968 ACGTTTCTTCTTATGCGCAACACAACTGCTGTGTGTTCTCTCTCTCTCTCTCTCT 1023

RESULT 4
US-08-592-936B-20
: Sequence 20, Application US/08592936B
: Patent No. 5783393
: GENERAL INFORMATION:
: APPLICANT: Kellogg, JILL A.
: TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR
: TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Denlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/592.936B
: FILING DATE: 29-JAN-1996
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Evans, Susan T.
: REGISTRATION NUMBER: 38,443
: REFERENCE/DOCKET NUMBER: 4257-0012

```

```

TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 324-0880
: TELEFAX: (650) 324-0960
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2917 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: Linear
: MOLECULE TYPE: DNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: sequence of the drul:PgIP chimeric
: INDIVIDUAL ISOLATE: gene
: US-08-592-936B-20

Query Match 17.1%; Score 170.8; DB 1; Length 2917;
Best Local Similarity 51.7%; Pred. No. 6.6e-45;
Matches 525; Conservative 0; Mismatches 467; Indels 24; Gaps 5;

Oy 2 tgaatattgaatcatctcttgcctatttggctatgcatgcatgatttctctgccttc 61
Db 1376 TCAATATCCCACTAATACATGCTTCAAGCTTAAGCATATTGTTGTCATCTTATCTT 1435
Oy 62 caaacctctctgcatacaaaagatgcacaacaacagcagaagcatttactcaaatca 121
Db 1436 TCAGAACTGCACTCTCAGAGCTATGCAACCCCAAGATAGCAAGCCCTTCTCAATCA 1495
Oy 122 aaacgaccttgaaaaaaccacatctacagactcagtggtgcagagcagatttgc 181
Db 1496 ACGAAACCTTGGCAACCAACCTCTCTTCATGGCTTCCAAACACCGACTTGTGA 1555
Oy 182 gttagagc---ctagtcgaatgtgacgaacagcagacgaataattccctcaatttc 238
Db 1556 ACAGAACTGGCTTAGGTGTTTATGCGACCGACACCAACCAATATGCGCTCAACAC 1615
Oy 239 aagaagcagaagctctcaacggccaa-----atcccaactcaagtggagagac 286
Db 1616 TCGACCTCTCCGGCCATTAACCTCCCAAAACCTTACCTATCTCTCTCTCTCTCTCT 1675
Oy 287 taccaactctcaagccttatgttgcgtlaaactcccaacttcttggaaaaatccca 346
Db 1676 TCCCTTACTCAATTTCTATCATTTGGCGGATCAATTAACCTGCTCGTCCAAATCCC 1735
Oy 347 aagaattctgcactcaagaacctaaatccctcagactcagctcagcagctcagtg 406
Db 1736 CCGCATGCTTAATCTCAACCTCACTATCTATATCTACACCAATGCTCTCG 1795
Oy 407 gccctgcccttatcttccctcagcttgaagaaacttaactgtttagactatcgltta 466
Db 1796 GCGCAATACCGGATTTCTTGTGCAGATCAAAACCTGTGACCTGACCTCTCTCTACA 1855
Oy 467 acaaaccttgggtgtaacccctcctcagcttccacttccagacttaagccctgc 526
Db 1856 ACGCCCTCTCCGGCACCCCTCCCTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1915
Oy 527 acttgaagcgttaagcagactcaggttgaatcccgatatttgggaatttgc---tg 583
Db 1916 CATTGACGCGAACCGAATCTCGGCGCCATCCCGACTCTACGGCTGTTTTCGAAGC 1975
Oy 584 gatcccgacacatalatcttcgcataaccagctccaggttcttcccaaaacttgc 643
Db 1976 TGTTTACGGGATGACATCTCCCGCAACCGCTCACGGGAAGATTCCACGACGTTTG 2035
Oy 644 ctgagcagatcccaattagtgctcagctctcagggagaagactagaagtgatattcat 703
Db 2036 CCAATCTGAACCTGGCGTTCTGTGACTTGTCTCGAACAATGCTGGAGGCTGCGCTGG 2095
Oy 704 tcttgcttggtcctaaaaacgcttggaaatgctgatttctcaggaacggtgtagt 763
Db 2096 TGTGTTTCGGGTCATGAAGAACAAGAAAGATATCATCTGGCAAGAACTCTCTCTT 2155

```


GENERAL INFORMATION:
APPLICANT: Cervone, Felice
APPLICANT: De Lorenzo, Giulia
APPLICANT: Salvi, Giovanni
APPLICANT: Albersheim, Peter
APPLICANT: Darvill, Alan
APPLICANT: Bergmann, Carl
TITLE OF INVENTION: Nucleotide Sequences Coding An
TITLE OF INVENTION: Endopolygalacturonase Inhibitor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sally A. Sullivan
STREET: 5370 Manhattan Circle Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,646
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 91A 000915
FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/IT/00158
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 19-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phaseolus vulgaris*
STRAIN: Pinto
IMMEDIATE SOURCE:
CLONE: PAD-1 (DSM NO. 57446926821)
FEATURE:
NAME/KEY: CDS
LOCATION: 2..685
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 686..792
US-08-244-646-16

Query Match 14.18; Score 140.4; DB 1; Length 792;
Best Local Similarity 53.5%; Pred. No. 2e-35;
Matches 363; Conservative 0; Mismatches 306; Indels 9; Gaps 3;

QY 325 aatcttctggaataatccagaagaattcttcgactccaagaaccctcaaatccctcaga 384
DB 5 AACCTCGTGGTCCATCCCGCCGCGTAACTCACTCCCACTCCACTATCTCTAT 64

QY 385 ctacagctcagcagctcagctgagccctgctcccttatcttcctccagctcagaacta 444
DB 65 ATCAACCCACCAATGCTCGCGGCGCAATACCCGATTCTGTCTCAAGATCAAAACCTC 124

QY 445 actgttaagactatcglttaacaactttgggtgtaatccctcagcttccact 504
DB 125 GTACACCTCGACTTCTCTACAAACCCCTTCGCGACCTTACCTCCATCTCTCT 184

QY 505 ctccgaaccttaagccctgcagcttagaagtaagcagaccacccgggaatcccgat 564
DB 185 CTCCCAACCTCGTAGAATCAATCGACGCAACCGAATCTCCGGCCATCCCCAC 244

QY 565 atcttgggaatttgc---cgaaccggagacatatacttcgcataaccagctcacc 621
DB 245 TCTACGGCTCATTTTTCACAGCTGTTCACGTGATGACATCTCCCGAACCGCTCAC 304

QY 622 gggttgttcccaaaactttgtctagagacagatccaaltgagctcgacttccaaggaa 681
DB 305 GGGAAGATTCCGCGCGCTTTCGAACTGAACCTGGCGCTTCTGACTTGTCTGAAC 364

QY 682 agactagaagtgatattatcttctgttgggacctaaagcgttggaaatctagat 741
DB 365 ATGCTGCAAGGTGACGCGCTCGTGTGTTGCGATCAGTAAGAACCCAGACATACAT 424

QY 742 ttctcaggaacagtgcttagtltcaattctccaggggtcagaggttccaccctcttg 801
DB 425 CTGCGAAGAACTCTCTCTGTTTGTGGAAGAACT---GGGCTGTCAAGAACTTG 481

QY 802 acatactagacttgaaccataaccagatcagcggaagtcgttgatgtgactaa- 860
DB 482 AACGGTGTGATCTGACGACACCGTATCTATGAGAGCTACCGACGAGCTACGAG 541

QY 861 --attgacccgcagacatttaagctcagtgatataatctcgcaggaagattccaaca 918
DB 542 CTAAAGTTTCTGCAAGTTTAAATGTAGCTTCAACATCTGTGGGTAATTTCTCAA 601

QY 919 gggggaacccctcagagatcagacggtacggcctatctccacaagcttctgtgtg 978
DB 602 GGTGGGAACCTTGCAACATTTTCAGTTCTGTCTTATGCAACAAAGTCTGTGTGT 661

QY 979 gctccattgccaagaatgc 996
DB 662 TCTCCTCTCTCTGCTGC 679

RESULT 7
US-09-180-439-5
Sequence 5, Application US/09180439
Patent No. 6225532
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
APPLICANT: Hatziathanis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
FILE REFERENCE: 620 - 53
CURRENT APPLICATION NUMBER: US/09/180,439
EARLIER FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
EARLIER APPLICATION NUMBER: GB 9619924.5
EARLIER FILING DATE: 1996-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 3541
TYPE: DNA
ORGANISM: *Lycopersicon esculentum*
US-09-180-439-5

Query Match 7.6%; Score 75.6; DB 4; Length 3541;
Best Local Similarity 48.2%; Pred. No. 2.7e-14;
Matches 275; Conservative 0; Mismatches 289; Indels 6; Gaps 2;

OY	251	cttcacgcggccaatccaccactcaggttgggagacccataccatcccaagccttatggt	310
Db	1567	ctcttatatggaactatccctgcttcattctgcgcacatatggaatactgcgaagctcctc	162
OY	311	tcgc taaacctccccaactcctttctcgaaanaatcccaagaagaattcttg bvt aaagacc	370
Db	1624	ttctccatgataaacaactctcatcttggggaaatctccttcatttgg tg caatttaacatcac	168
OY	371	taaaatccctcagaactcagctcgaccagctctcagtcgtgcccgtcccttatctctccctc	430
Db	1684	tagaacctgtgtatatacgagaaacaactttgaaggaaagtccgaatgtttgggtta	174
OY	431	agcttaagaaactaacttg tt tagactat cgt tt aacaaactttgggt ta ccctc	490
Db	1744	atatacgtgacctcttcggtttt tc caatg tca ctata tg tt cag tgg ag ag ccctc	180
OY	491	ctcagcttctccactcttcgcgaaccttaaaagccctgacttagaacgtaacgaaactcacg	550
Db	1804	cactatcttccaatttaactacactccataaataactctgattttggcaaaacaactctggagg	186
OY	551	gtgaatcccccga at ct tt gggaat tt gt tga tcc ccg ga catat ct tc cata	610
Db	1864	gagcaatcacacaatgtttgggaatataagtagcctccaggtttttgata gc gaata	192
OY	611	accgcgc cca cgg gt t gt t cc caaaa ct t tg c tag ag aga t cca	667
Db	1924	acaaactcttgggaactctccacaacaaatttagctattgattgttcaactgataagtcca	198
OY	668	actctc tga gga cag act cga gga gg at t cat ct c gt t t gg c t aa aaa ac t	727
Db	1984	acttgc at cgt c caat tg aat c tag aga t g aaat cc ct t g c t t t g ga ca at t g ca aa a gc	204
OY	728	tggaat t g c at g at t t c a g ga aa c t g c t a t t t c at t c c c a g g t c a g g at	787
Db	2044	tgcaagt ct t g at t t a g a g a c a at c a a c a a c a g c a c at t c c at t g t t g g aa	210
OY	788	ttccaccctctt g a c a t a c t a g a c t t ga	817
Db	2104	ctttgc c g a g c t g a g at t t aa gt t ga	2133

```

US-09-180-439-1
RESULT 8
: Sequence 1, Application US/09180439
: Patent No. 6225532
: GENERAL INFORMATION:
: APPLICANT: Dixon, Mark S
: APPLICANT: Hatzixanthis, Kostas
: APPLICANT: Jones, David A
: APPLICANT: Jones, Jonathan DG
: TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
: FILE REFERENCE: 620 - 53
: CURRENT APPLICATION NUMBER: US/09/180,439
: CURRENT FILING DATE: 1998-12-06
: EARLIER APPLICATION NUMBER: PCT/SB97/01249
: EARLIER FILING DATE: 1997-05-08
: EARLIER APPLICATION NUMBER: GB 9609681.3
: EARLIER FILING DATE: 1996-05-09
: EARLIER APPLICATION NUMBER: GB 9619924.5
: EARLIER FILING DATE: 1996-09-24
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3979
: TYPE: DNA
: ORGANISM: Lycopersicon esculentum
: US-09-180-439-1

```

Query Match	7.2%;	Score 71.8;	DB 4;	Length 3979;
Best Local Similarity	49.6%;	Pred. No. 4.7e-13;		
Matches 212;	Conservative 0;	Mismatches 212;	Indels 3;	Gaps 1;

OY	334	accacgtccagctggccctggccccttcttctccctcagcttagcgaataactctgttta	453
Db	2262	aacaattttagaagggaanaagttccgcgaatgtcttggtaatacagtgaaacttcaacatttg	2321
OY	454	gactatcgttttaacaaacttttgggtgtaatccctccctccagcttccactctccgaac	513
Db	2332	tcgagtgcattcattagtcttccagggagctccctccatcattcttccatttcaacatca	2381
OY	514	cttaagccctcgcccttagaagcgttaagaaactaacccggtgaaatcccgatctcttgg	573
Db	2382	ctaaaaaactctgttcttggcaganaaaactctggaggcgacatacacaacttcttggc	2441
OY	574	aatttcgtgaatcccccgcgaacataatcttgcataaccagctaacccgggttcttccc	633
Db	2442	aatacttgtagcccccacgggttcttgatagcgaataaacaactcttcggagctcttcca	2501
OY	634	aaaacttgcctagagacatacca--atbagctcgaactcttcaggggaacagactaga	690
Db	2502	acaacttttagcatgtgattgtcttcacgataagcttcaacttcatlgtgcgaatgaatagca	2561
OY	691	ggtaatttcattctctgtttgggcctaaaaaacgtcttgaaatgctagatlttccaga	750
Db	2562	gattgaatcccttcggtcttcttggacaattgcgaanaagctgcaagttcttgatttagagac	2621
OY	751	aaagctgtatgtattcaattcttcctcagaagtgacagagattccacccctcttgaacatca	810
Db	2622	aatcaactcaagacgaacatttcccatcagtggttgggaacttcccgagactgagagtttca	2681
OY	811	gactttga 817	
Db	2682	aggtttga 2688	

```

RESULT          9
: Sequence 2, Application US/09180439
: Patent No. 6225532
: GENERAL INFORMATION:
: APPLICANT: Dixon, Mark S
: APPLICANT: Hatixanthis, Kostas
: APPLICANT: Jones, David A
: APPLICANT: Jones, Jonathan DG
: TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
: FILE REFERENCE: 620 - 53
: CURRENT APPLICATION NUMBER: US/09/180,439
: CURRENT FILING DATE: 1998-12-06
: EARLIER APPLICATION NUMBER: PCT/G97/01249
: EARLIER FILING DATE: 1997-05-08
: EARLIER APPLICATION NUMBER: GB 9609681.3
: EARLIER FILING DATE: 1996-05-09
: EARLIER APPLICATION NUMBER: GB 9619924.5
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 3979
: TYPE: DNA
: ORGANISM: Lycopersicon esculentum
: US-09-180-439-2

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	Query Match	7.2%	Score 71.8	DB 4	Length 3979
	Best Local Similarity	49.6%	Pred. No. 4.7e-13		
	Matches 212	Conservative	0	Mismatches 12	Indels 3
					Gaps 1
QY	394	accagctccagttgcccgtcccttattctctccctcagcttcaagaacaaactgttta	453		
Db	2262	aacacatttgaagggaagaagcttcgcgaatgtttggttaatatcagtgaccttcacattt	2321		
QY	454	gacttattgttttaacaacactttgggtgttaatccctccctcagcttccacacttccgaac	513		
Db	2322	tccgattccatcatatagtttcagaggaagagctccctcatcatcattccaatttaacatca	2381		

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OY 514 cctaaagccctgacttagaagcgaacccaccggtgaaatccccgatatcttggg 573
  |||||
DB 2382 ctaaaatattgatttggcagaaacatctggaggcggaatacacaatttctggc 2441
OY 574 aatttgcggttcccggaacatatcttgcataaacagctcaacgggttctcc 633
  |||||
DB 2442 aatatagtagccctcaggttcttgatagcagaataaacaacttctggactctcca 2501
OY 634 aaacttgcctagagcaacatcca---attaagctcagacttccagggagacataga 690
  |||||
DB 2502 acaaatattagatgtagtgcactgataagttcctaacttgcagggacatgaataga 2561
OY 691 ggtgatatcttcttcttgggtccctaaagcgttgaaatgctagatttccaga 750
  |||||
DB 2562 gatgaatccctcgcttcttgacaattgcaaaagctgcaagcttcttgatagagac 2621
OY 751 aacgtgcttagttcaattctccaggggtgcagaggttccacccctcttgacatacta 810
  |||||
DB 2622 aatcaactcaacgacacattcccatgtgtgtggaacttgcagagctgaggtttta 2681
OY 811 gacttga 817
  |||||
DB 2682 aggttga 2688

RESULT 10
US-09-180-439-7
: Sequence 7, Application US/09180439
: Patent No. 6225532
: GENERAL INFORMATION:
: APPLICANT: Dixon, Mark S
: APPLICANT: Hatzixanthis, Kostas
: APPLICANT: Jones, David A
: APPLICANT: Jones, Jonathan DG
: TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
: FILE REFERENCE: 620 - 53
: CURRENT APPLICATION NUMBER: US/09/180,439
: EARLIER FILING DATE: 1998-12-06
: EARLIER APPLICATION NUMBER: PCT/GB97/01249
: EARLIER FILING DATE: 1997-05-08
: EARLIER APPLICATION NUMBER: GB 9609681.3
: EARLIER FILING DATE: 1996-05-09
: EARLIER APPLICATION NUMBER: GB 9619924.5
: EARLIER FILING DATE: 1996-09-24
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: Patentlin Ver. 2.0
: SEQ ID NO 7
: LENGTH: 4123
: TYPE: DNA
: ORGANISM: Lycopersicon esculentum
US-09-180-439-7

Query Match 7 2% Score 71.8: DB 4: Length 4123:
Best Local Similarity 49.6%: Pred. No. 4.8e-13:
Matches 212: Conservative 0: Mismatches 212: Indels 3: Gaps 1:
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```
OY 634 aaacttgcctagagcagatcca---attagctgacttctcagggaacagactaga 690
  |||||
DB 2646 acaaatattagatgtagtgcactgataagttcctaacttgcaggaatgaactaga 2705
OY 691 ggtgatatcttcttcttgggtccctaaagcgttgaaatgctagatttccaga 750
  |||||
DB 2706 gatgaatccctcgcttcttgacaattgcaaaagctgcaagcttcttgatagagac 2765
OY 751 aacgtgcttagttcaattctccaggggtgcagaggttccacccctcttgacatacta 810
  |||||
DB 2766 aatcaactcaacgacacattcccatgtgtgtggaacttgcagagctgaggtttta 2825
OY 811 gacttga 817
  |||||
DB 2826 aggttga 2832

RESULT 11
US-09-353-585-4
: Sequence 4, Application US/09353585
: Patent No. 6287865
: GENERAL INFORMATION:
: APPLICANT: Dixon, Mark S
: APPLICANT: Jones, David A
: APPLICANT: Jones, Jonathan DG
: TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Nixon & Vanderhye PC
: STREET: 8th Floor, 1100 No. 6287865th Glebe Road
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22201-4714
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentlin Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/353,585
: FILING DATE: 15-Jul-1999
: CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12O 1/68
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/930,277
: FILING DATE: 27-OCT-1997
: APPLICATION NUMBER: PCT/GB96/00785
: FILING DATE: 01-APR-1996
: APPLICATION NUMBER: GB 9506658.5
: FILING DATE: 31-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Ms Mary J Wilson
: REGISTRATION NUMBER: 32,955
: REFERENCE/DOCKET NUMBER: 620-69
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 816-4000
: TELEFAX: (703) 816-4100
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3573 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Tomato
: STRAIN: Cf2
: SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Db 4151 TCCTTACCGCAATCGGAACATGACGAGTTTAACTCTCGATCTCTTTTCAACGATC 4210
QY 617 tcacgggttcttcc 632
Db 4211 TCTCCGGTAGATACC 4226

RESULT 15

US-08-567-375-3
Sequence 3, Application US/08567375
Patent No. 5952485

GENERAL INFORMATION:

APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Confering
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 023070-058930

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS: 1

LENGTH: 3921 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: join(1..2676, 3520..3918)

OTHER INFORMATION: /product= "Xa-21"

US-08-567-375-3

Query Match

Best Local Similarity 4.7%: Score 46.8: DB 2: Length 3921:

Matches 150: Conservative 0: Mismatches 172: Indels 0: Gaps 0:

QY 373 aaatccctcagaactcagctcgaccagtcagtcgcccctccttattctcctcag 432
Db 1207 CAACATCTCTATCTCTGCAACAACAAATTTGAGAGGGCTCTTCATCATCTGTTGGGAGG 1266
QY 433 cttaagaaactaactglttagacttalcgtttaaacttttggttgaatccctcc 492
Db 1267 CTTAAANAACCTTAGGCATTTCTACTGCGCTACGAANAACACTTGAGCGGTTTGATCCGTTG 1326
QY 493 cagcttccacitctccgaacctaaagccctgacacttagaagcgtlaacgactcaccgt 552
Db 1327 GCCATAGGAATCTTACTGAACTTAATATCTTACTGCTCGGACCAACAATTCAGTGT 1386
QY 553 gaaatcccgatattcttgggaatttgcgcgaatcccgacataatcttcgataac 612
Db 1387 TGGATACCATACACACTCTCAACCTCACAACTGTGTTCATTAGCCCTTCAACTAAT 1446
QY 613 cagctcaccgggttcttccca 634
Db 1447 AACCTTAGTGTCCAAATACCA 1468

Search completed: March 13, 2002, 20:14:05
Job time: 2656 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 18:35:44 ; Search time 1172.24 Seconds
(without alignments)
9157.709 Million cell updates/sec

Title: US-09-308-140-6

Perfect score: 999
Sequence: 1 atgaataatgaaccatctt.....ctccatgcagaatgctag 999

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 segs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estfun:*
2: em_estln:*
3: em_estln:*
4: em_estln:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hlc:*
10: gb_estl:*
11: gb_est2:*
12: gb_hlc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vtl:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	203.2	20.3	644	11	BG577452 P23 MP12-
2	202	20.2	742	11	BG127791 EST473437
3	190.8	19.1	626	10	AW217580 EST296294
4	188.8	18.9	573	10	AW928759 EST337547
5	188.4	18.9	647	10	AW737407 EST338750
6	187.4	18.8	569	10	AW217650 EST296364
7	186	18.6	584	11	BF270811 GA_Eb000
8	177.4	17.8	548	10	AT730245 BNLGH1646
9	174.4	17.5	533	11	BG132344 EST465236
10	173.4	17.4	546	10	BE459449 EST414741
11	173.4	17.4	781	11	BG587815 EST489590
12	164.4	16.5	640	10	AW776847 EST335912

13	161	16.1	635	11	BF003501	BF003501 EST431999
14	160	16.0	587	10	AV542271	AV542271
15	157.6	15.8	517	10	BE463191	BE463191 EST354414
16	153.8	15.4	513	10	AW624693	AW624693 EST322638
17	152.8	15.3	663	11	BG441226	BG441226 GA_Ea001
18	152.8	15.3	888	11	BG441233	BG441233 GA_Ea001
19	152.6	15.3	569	10	A1507686	A1507686 sb10c11.Y
20	150.4	15.1	517	10	AW398215	AW398215 EST298062
21	142.6	14.3	590	10	AW585990	AW585990 EST317613
22	140.4	14.1	639	11	BF424032	BF424032 s11e04.Y
23	139.6	14.0	557	10	AV549913	AV549913 AV549913
24	138.8	13.9	602	11	B1207435	B1207435 EST525475
25	138.8	13.9	740	11	B1208875	B1208875 EST526915
26	138.2	13.8	515	11	BG598941	BG598941 EST503841
27	136.8	13.7	453	10	AW929041	AW929041 EST337745
28	135.8	13.6	579	10	AV542007	AV542007 AV542007
29	132.2	13.2	483	11	C95367	C95367 C95367 C1tr
30	129	12.9	569	10	AV549817	AV549817 AV549817
31	122	12.2	635	11	B1405301	B1405301 116B11 Ma
32	121.6	12.2	652	11	BF068634	BF068634 s112f03.Y
33	120.6	12.1	573	11	BF054100	BF054100 EST439330
34	119.4	12.0	416	10	BE022733	BE022733 sm87909.Y
35	116.8	11.7	601	11	B1210636	B1210636 EST528696
36	113	11.3	826	11	BG582432	BG582432 EST484176
37	112.6	11.3	614	11	BE979949	BE979949 EST429672
38	111.4	11.2	430	10	AV411355	AV411355 AV411355
39	111.2	11.1	427	10	AV411106	AV411106 AV411106
40	111.2	11.1	657	10	AW686216	AW686216 NF03906N
41	110.2	11.0	487	11	BF070747	BF070747 s124509.Y
42	107.2	10.7	596	11	BG405813	BG405813 sac3807.Y
43	106.6	10.7	469	10	A1938190	A1938190 sc40603.Y
44	106.6	10.7	511	10	AV535415	AV535415 AV535415
45	106.6	10.7	538	10	AV531396	AV531396 AV531396

ALIGNMENTS

RESULT 1
BG577452
LOCUS BG577452 644 bp mRNA EST 05-JUL-2001
DEFINITION P23 MP12-ADIS 006 Lambda Zap II library Beta vulgaris cDNA similar to polygalacturonase inhibitor precursor, mRNA sequence.
VERSION BG577452
KEYWORDS BG577452.1 GI:14602746
SOURCE EST.
ORGANISM Beta vulgaris.
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Chenopodiales; Beta.

REFERENCE
AUTHORS Schneider,K., Weisshaar,B., Borchardt,D.C. and Salamini,F.
TITLE SNP frequency and allelic haplotype structure of Beta vulgaris expressed genes
JOURNAL Unpublished (2001)
COMMENT Contact: Schneider K

ADIS unit
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Tel: 00492215062404
Fax: 00492215062413
Email: kschneider@piz-koeln.mpg.de
basis for pgin marker in sugar beet.
Location/Qualifiers
1. 644
/organism="Beta vulgaris"
/db_xref="taxon:161934"
/clone_lib="MP12-ADIS 006 Lambda Zap II library"
/dev_stage="4 week old pot-grown plants"
/note="Organ: shoot and root; Vector: Bluescript; cDNA was ligated to a 15-mer oligonucleotide adaptor (Stratagene) and cloned into the EcoRI site of the Bluescript plasmid"

FEATURES

source

[illegible][illegible]

Db 394 CAGGTCGCATCCCTGAAATTCCTTAGTCAGCTGGAAGAAATTTGACGTGGCTGCAGTTGAAATT 453
 Qy 464 ttaacaacattcttggtgtaactccctccagcttccacctcttcgaaacctaaagccc 522
 Db 464 ACAATCAATTTACCGGAGCAATTCCTCTTCCCTCTCTCAAGCTTCCCAATTTGCTTACGGA 513
 Qy 524 tgcacttgaacgctaaacgaactcaccggtgaatcccgatctccttggaaatttgcg 583
 Db 514 TGTACTTAGATCGTACCAACTCTCACCGGAGACAATACCGGAATCGCTTTGGGAGATTTAAG 573
 Qy 584 gatc-----cccgacataatcttccgacaaacgaactcaccggttctgt 629
 Db 574 GACCAAAATATCCAGATCTCTACTCTTTACACCAACACACTTGACCGGACATGT 625

RESULT	4
LOCUS	AM928759
DEFINITION	AM928759 573 bp mRNA EST 18-MAY-2001
VERSION	EST333547 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum cDNA clone CTC03C9 5', mRNA sequence.
KEYWORDS	AM928759
SOURCE	AM928759.1 GI:8104154
ORGANISM	EST. tomato. Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 573) van der Hoeven,R.S., Bezzerides,J.L., Matern,A.L., Holt,I.E., Jiang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Roming,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue Unpublished (1999) Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

	FEATURES	Location/Qualifiers
	Source	1..573
		/organism="Lycopersicon esculentum"
		/cultivar="TA96"
		/db_xref="taxon:4081"
		/clone="CTOC3c9"
		/clone_lib="tomato flower buds 8 mm to pre-anthesis, Cornell University"
		/tissue_type="flower"
		/dev_stage="buds 8mm-to-preanthesis"
		/note="Vector: pluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: TANKSLey; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA96). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
BASE COUNT	171 a	142 c
ORIGIN	97 g	163 t
Query Match	18.9%; Score 188.8;	DB 10; Length 573;
Best Local Similarity	60.8%;	Pred. No. 2.6e-44;
Matches 326;	Conservative 0;	Mismatches 207; Indels 3; Gaps 1
QY	44 tgatttcctgcgtccccaacactctctgcatcacaaagaatggcaacaacagcagaagg	103
DG	37 tatattttcttgcttggcttgtctcttcacacnaccagnatgcgaatgccaaccaagacaaaaa	96
QY	104 aaagcttacctcaaatcaaacaacagccttgaaaacccccaccatcacagactcattyggigt	163
DG	97 AAGTCCCTTCACAAATATAAGAACAAGCATGGCAATCCTTAGCCATTAGCTTGCGGATC	156

Db 475 AGCTCCCTTAAACACTGCCAATCTCGAGGCTTTCATTTGGATAGAAACAAGTAACACT 534
|||||
Oy 550 ggtgaatccccgatalacttgggaatttgcgtg 584
|||||
Db 535 GGTAACATACCAAGATCTTTGTGTATGTTCTAG 569
|||||
RESULT 8
AT1730245 548 bp mRNA EST 11-JUN-1999
LOCUS BNLGH16465 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
DEFINITION to (AB013397) polygalacturonase inhibitor [Citrus jambhiri], mRNA
sequence.
ACCESSION AT1730245
VERSION AT1730245.1 GI:5049097
KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 548)
AUTHORS Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
TITLE ESTs from developing cotton fiber
JOURNAL Unpublished (1999)
COMMENT Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burrb@bnl.bnl.gov
Seq primer: T3 Primer.
Location/Qualifiers
FEATURES
source 1..548
/organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="Immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Vector: pBluescript II KS-"
BASE COUNT 137 a 174 c 82 g 155 t
ORIGIN
Query Match 17.8%; Score 177.4; DB 10; Length 548;
Best Local Similarity 60.5%; Pred. No. 5.5e-41;
Matches 292; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

Db 363 CTCAGACGCTTGCTGACCTGACCAATCTTCCGCTCAGTCCCTAATTTTTCAGC 422
|||||
Oy 430 cagcttaccgaactacttlttagactatcgtttacaactlttgggtgaatccct 489
|||||
Db 423 CAAGTTAGAACTTGAATCTTGTGACCTTCAATTAATACCTCTCGGATCTATTC 482
|||||
Oy 490 cctcagcttccactctccgaacttaagccctgcacttagaagtgtaacacc 549
|||||
Db 483 AGCTCCCTTCAACACTGCCAATCTCGATGCTTTCATTTGATGAAACAAGTAAC 542
|||||
Oy 550 ggt 552
|||||
Db 543 GGT 545
|||||
RESULT 9
BG132344 533 bp mRNA EST 31-JAN-2001
LOCUS BG132344
DEFINITION EST465236 tomato crown gall Lycopersicon esculentum cDNA clone
C70E7C12 5' sequence, mRNA sequence.
ACCESSION BG132344
VERSION BG132344.1 GI:12632532
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 533)
AUTHORS van der Hoeven, R., Sun, H., Cho, J., Utterback, T., Hansen, C., Romning
C. and Tanksley, S.
TITLE Generation of ESTs from tomato crown gall tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
Location/Qualifiers
FEATURES
source 1..533
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="C70E7C12"
/clone_lib="tomato crown gall"
/tissue_type="crown gall"
/dev_stage="crown galls from full-grown plants (8 wks old)"
/lab_host="SOLR"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI. Four wk old greenhouse plants were stab inoculated
on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr,
Cornell U.). Galls were allowed to develop for another 4
wks, when gall tissue was frozen in liquid nitrogen."
BASE COUNT 156 a 136 c 86 g 155 t
ORIGIN
Query Match 17.5%; Score 174.4; DB 11; Length 533;
Best Local Similarity 60.5%; Pred. No. 4.1e-40;
Matches 305; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	TITLE	JOURNAL	COMMENT
DB	153	CAAACACGATTGCTGTACTGGTAGCTGTAATAATGTTCAGCGAANAACCAACGCGATTA	212						
OY	224	ttccctcataatcacaagcagcgaagctcaccggccaabcccaactcagtgagg	283						
DB	213	ATGCTCTCACCGCTTTCACAGCCAA--TATCTCCGGCCAAATTCGGCGAGCGTCGGAG	269						
OY	284	accacatactaccgaagccttatggtccgtaactcccaactctttggaaaaac	343						
DB	270	ACCTTCATATCTGGAACAACTTGGAATTCATCATCTACTATCTCACCGGAACAATTC	329						
OY	344	cagaagaatctcgcacataaagactaaacccctcagactcagctcgacagctcca	403						
DB	330	CACGTGCATTTGCCAAGCTCACAATCTCAAAATGTTAAGGCTCAGCTTCATCACTTA	389						
OY	404	gtggccctgcctccttatctctccctcagcttaacgaactaactgtttagactatcgt	463						
DB	390	CAGTCCGATCCCGAATTCCTTAGTCAGCTCAAGCAATTTGACGTTGCGAGTTGAAT	449						
OY	464	ttacaacatttggtggtatcccccctcagcttcccaactcttcgaacctaagccc	523						
DB	450	ACAATCAATTTACCGGAACATCCCTTCTTCCTCTCTCAGCTCCGATTTGCTAGCGA	509						
OY	524	tgcaactagaacgtaagaactca	547						
DB	510	TGTACTTAGATCGTAACAACCTCA	533						
RESULT	10								
LOCUS	BE459449	546 bp	MRNA	EST	18-MAY-2001				
DEFINITION	EST414741 tomato developing/immature green fruit Lycopersicon								
ACCESSION	BE459449								
VERSION	BE459449.1	GI:9503751							
KEYWORDS	EST.								
SOURCE	tomato.								
ORGANISM	Lycopersicon esculentum								
REFERENCE	Alcala,J., Vrbalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,								
AUTHORS	liang,F., Hansen,T.S., Creaven,M.B., Bowman,C.L., Rønning,C.M.,								
	Nieman,M., Fraser,C.M., Martin,G.B., Giovannoni,J.V. and Tanksley								
	S.D.								
	Generation of ESTs from tomato fruit tissue, immature green								
	unpublished (2000)								
TITLE	unpublished (2000)								
JOURNAL	Clemson University Genomics Institute								
COMMENT	Clemson University								
	100 Jordan Hall, Clemson, SC 29634, USA								
	Email: http://www.genome.clemson.edu/orders/index.html								
	5 prime sequence.								
FEATURES	Location/Qualifiers								
source	1..546								
	/organism="Lycopersicon esculentum"								
	/cultivar="TA496"								
	/db_xref="taxon:4081"								
	/clone="CLEM6H18"								
	/clone.lib="tomato developing/immature green fruit"								
	/tissue.type="fruit"								
	/dev.stage="immature green (5-35 days post-anthesis)"								
	/lab.host="SOLR"								
	/note="vector: pBluescriptSKMcuNadapT, site_1: EcoRI,								
	site_2: XhoI; Fruit were tagged at 5 dpa (0.5 cm) and								
	harvested at 7 day intervals through 35 dpa. Equal mass								
	of tissue from each stage were combined (including seeds								
	and locales) prior to mRNA isolation."								
BASE COUNT	156 a	140 c	98 g	152 t					

Query Match	17.4%	Score 173.4	DB 10	Length 546
Best Local Similarity	59.9%	Pred. No. 8.1e-40		
Matches 329	Conservative	0	Mismatches 211	Indels 9
Gaps				2
Qy	164	cagaagacattgttctgttggagacctagtcgaagtgtacgaagaacacagccagcataa	223	
Db	1	CNAACACAGATTGCTGTACTCTGTACGTGTGAATGTAATGTAACCGGAACCAACGCGATGA	60	
Qy	224	ttccctcaataatcgaagcgaagcgtctcacccggccaatcccaacctcaggttgag	283	
Db	61	ATGCTCTCACCGCTTCTCCAGCCAA---TATCTCCGGCCCAAAATTCGGCAGCGCTGGAG	117	
Qy	284	acctccactaccctcaagcctatagtttcgcgtaactcccccaatctttcggaaaatcc	343	
Db	118	ACCTTCATATCTCGAAMCATTTGATTCATATGTTACTATCTACCGCAACAAATTC	177	
Qy	344	cagaagaattctctgcactcaagaacctaaatccctcagactcagctcagacagctca	403	
Db	178	CACCTGCAATTGCGAAGCTCACAAATCTCAAAATGTTAAGGCTCAGCTTCACTAACCTTA	237	
Qy	404	gtgcctcgtcccttatctctccctcagcttcaagaactcgtgtttagactatcgt	463	
Db	238	CAGGTCGCAATCCCTCAATCTCTTAGTCACCTCAAGAAATTTGACGTTGCGAGTTGAAT	297	
Qy	464	ttaacaaccttttggtgtgaatccctccctcagctcttccactccctccgaaccttaagcc	523	
Db	298	ACAATCAATTTACCGGACAAATCCTTTCTCCCTCTCTAGCTTCCGAATTTGCTAAGCA	357	
Qy	524	tgcacttgaagctgaacgaactcacccgggtgaatcccgatatactttggaattctgctg	583	
Db	358	TGTACTTGATGCTGAACAACTCACCGGAACTACCGGAATCGTTTGGAGATTTAAAG	417	
Qy	584	gatc-----ccggacatatatctttgcataaaccagctccccgggtgttctcccaaa	637	
Db	418	GACCAATATACCAATCTCTTACACACACAGCTTGACCGGACATGTGCGCGCT	477	
Qy	638	ctttgctcagagcagatccaattagctctcagctcttcagaggaacagactagaagtgata	697	
Db	478	CTTTAGTGATTTGTAATTTTTCACAGGCTTGATTTCTCCAGAAATAGCTTGAAGGAGATG	537	
Qy	698	ttcaatcct 706		
Db	538	TTTCGTTTT 546		
RESULT 11				
LOCUS	BG587815	781 bp	mRNA	EST
DEFINITION	EST4895590 MHAM Medicago truncatula/Glomus versiforme mixed EST			11-APR-2001
ACCESSION	BG587815			
VERSION	BG587815.1	GI:13602879		
KEYWORDS	EST.			
SOURCE	Medicago truncatula/Glomus versiforme mixed EST library.			
ORGANISM	Medicago truncatula/Glomus versiforme mixed EST library			
REFERENCE	1 (bases 1 to 781)			
AUTHORS	Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Unterback,T., Cho,J.			
TITLE	and Fraser,C.M.			
JOURNAL	ESTs from roots of Medicago truncatula after colonization with			
COMMENT	Glomus versiforme, 2001			
	Unpublished (2001)			
	Contact: Harrison M.J.			
	Plant Biology Division			
	The Samuel Roberts Noble Foundation			
	2510 Sam Noble Parkway, Ardmore, OK 73401			
	Tel: 580-223-5810			
	Fax: 580-221-7380			
	Email: mharrison@noble.org			
	Noble EST name: N386888e TIGR sequence name: MTDDK897K More			
	information is available at: http://www.medicago.org			
	Seq primer: Skmod (CTA gaa cta gtc gat cc).			

FEATURES
SOURCE

Location/Qualifiers

1. 781 /organism="Medicago truncatula/Gloms versiforme mixed EST

/library="Medicago truncatula genotype A17"

/db_xref="taxon:119092"

/clone="PMHAM-5109"

/clone_1ib="MHAM"

/tissue_type="roots colonized with Gloms versiforme"

/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days

post-inoculation with Gloms versiforme. The library was

made from a mixture of RNA from each of these stages."

/lab_host="E. coli strain XLOLR"

/note="Vector: Bluescript SK-; Site.1: EcoRI; Site.2:

XhoI; cDNA was prepared from polyA+ enriched RNA from

roots harvested at 10, 17, 22, 31 and 38 days

post-inoculation with Gloms versiforme. The cDNA was

directionally ligated into the UniZap XR vector from

Stratagene and packaged using Gigapack III Gold packaging

extracts. Plasmids containing cDNA inserts were excised

from the recombinant lambda-Zap phage using Ex-assist

helper phage and propagated in XLOLR cells."

BASE COUNT 215 a 236 c 128 g 202 t
ORIGIN

Query Match 17.4%; Score 173.4; DB 11; Length 781;

Best Local Similarity 55.8%; Pred. No. 9e-40;

Matches 419; Conservative 0; Mismatches 316; Indels 16; Gaps 4;

29 ttgtgcatatgatgatgttctctcgtcccaaacctctcgtatcaaaagatga 88

27 ttctatctcttcttcttcttcttcttcttcttcttcttcttcttcttctt 86

89 acaacaagacaagaagcttacttcaataaacaagccttgaaaacccacatta 148

87 accacacagacagaggtcttcttcttcttcttcttcttcttcttcttctt 146

149 cagactatgggtgtagcagcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 208

147 tagcctatggagaccacacacagatgtgtgtgtgtgtgtgtgtgtgtgtgt 206

209 ccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 259

207 taac 266

260 gccaaatcccaactcaagtgtagcagcagcagcagcagcagcagcagcagc 319

267 gcaactatcccccctttagtgtagcagcagcagcagcagcagcagcagcagc 326

320 tcccaactcttgcgaataatcccaagaagaattctgcactcaaaagacataatccc 379

327 tccccagcgttcmaagggcccaatccagccacacacacacacacacacacac 386

380 tcagacccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 439

387 ttttcatattgataacacatgtctcagggccgataccacacacacacacacac 446

440 aactaactgtttagacttgcgttcaacaacttctgtgtgtgtgtgtgtgtgtgt 499

447 accctcagcgttttcttcttcttcttcttcttcttcttcttcttcttcttct 506

500 ccaactcttgcgaacttaaaagccctgagcagcagcagcagcagcagcagcagc 559

507 cagacgttaccacttcttcttcttcttcttcttcttcttcttcttcttcttct 566

560 ccgatactcttgggaatttgcgcgatacccgacacatactc-----tttcgataaaccag 615

567 caga-atcattcgttcttcttcttcttcttcttcttcttcttcttcttcttcttct 625

616 ctacacgggtgttcttcccaaaacttctgttagagcagatccaaattagcctgtctca 675

626 ctctctggggcccatctccagccttattagctcaaatagatccacaaagaaatagactgtctg 685

Qy 676 gggacagcagtagaagtgat--attcatctgtgttggccttaaaaacgcttgga 733
 Db 686 AGGACAGCCTTGAAAGGGGATGCCCTTGCTTGGAGAGCCAGAAAGACACAAAT 745
 Qy 734 tgcagatcttccaggaagcgttgatgtt 764
 Db 746 ACTTTGATGTTTCTAGGACCTTGTTCTTT 776

RESULT 12

AM776847

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 640)
 Fedorova, M., Peterson, B.L., Samac, D.A., Vance, C.P., Gant, G.S., Peng,
 H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S.,
 Holt, I.E., and Fraser, C.M.
 ESTs from leaves of Medicago truncatula after inoculation with
 Colletotrichum trifolii
 Unpublished (2000)
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 Tel: 612 625 1243
 Fax: 651 649 5058
 Email: debys@pccn1.crl.umn.edu
 Minnesota sequence name: M260443e
 TIGR sequence name: M260443e
 More information is available at:
 http://chryslie.tamu.edu/Medicago
 Seq primer: SKmod (CTA gaa CTA gta gat CC).
 Location/Qualifiers
 1. 640
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"
 /clone="pDSIL-1668"
 /clone_1ib="DSIL"
 /tissue_type="leaves infected with Colletotrichum
 trifolii"
 /dev_stage="cotyledons and primary leaves harvested 5 and
 8 days after inoculation with Colletotrichum trifolii"
 /lab_host="E. coli strain XLOLR"
 /note="Vector: Bluescript SK-; Site.1: EcoRI; Site.2:
 XhoI; cDNA was prepared from polyA+ enriched RNA from
 cotyledons and primary leaves harvested 5 and 8 days after
 inoculation with Colletotrichum trifolii. The cDNA was
 directionally ligated into the Uni-ZAP XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-Zap phage using Ex-assist
 helper phage and propagated in XLOLR cells. Note: EST may
 be of fungal origin."

FEATURES

SOURCE

BASE COUNT 181 a 207 c 103 g 149 t
ORIGIN

Query Match

Best Local Similarity 16.5%; Score 164.4; DB 10; Length 640;

Matches 362; Conservative 0; Mismatches 256; Indels 14; Gaps 3;

QY 95 acgaagaagcaagcttctcaaatcaaaagccttgaaaacccaccattacagact 154
 Db 3 AAGCAAGAGGGCCCTCTCCATCAAGAAAGAACTCAACACCTTATCTTACCT 62
 QY 155 catggtgtcagaagcagatgtgtgtgtgagcctcagcgaatgtgagcaacagca 214
 Db 63 CATGGAGCCACAGACAGATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 122
 QY 215 accgcaataattccctcaataatcaaac-----gacgaagcctcagcgccaaa 265
 Db 123 ACCGTATCACTGCTCCATATGCAATCTCCGTCAGACACAAATCTCTCAGGCACTA 182
 QY 266 tcccaacagcagtggtgagcagctaccacacacacacacacacacacacacacac 325
 Db 183 TACCCCTTCACTGCTGAGACCTCCCTTATCTTGAANAATCTCGAATTCACAACTCCCA 242
 QY 326 atcttctcgaaaataaccagaaagaaattctgcactcaagaactaaatccctcagac 385
 Db 243 GGCCTCAAGGGCCCAATCCAGCCCACTATCGCAAGCTCAGAAACTCAGATCTTTTCA 302
 QY 386 tcagctcagcagcagctcagtggtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 445
 Db 303 TTGAATACACCAATGCTCAGGCGCATACACCTTCTTGCCCACTTAAACCTTCC 362
 QY 446 ctgttgaagcttctgtttaaacaacttgggtgtgtgtgtgtgtgtgtgtgtgtgtgt 505
 Db 363 AGCTTCTTCACTTCAACACCACTCTCAGCCGATCCCAAGCTCACTTCTTACAGC 422
 QY 506 ttcgaacctaaagccctcagcacttgaagcagcagcagcagcagcagcagcagcagc 565
 Db 423 TACTTACCTTGAATCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 481
 QY 566 tcttgggaatttgcctcagcagcagcagcagcagcagcagcagcagcagcagcagc 621
 Db 482 TCATTCGCTTCTTCAAAAAGCCGCGCATATCTTATCTTCAACACCACTTCT 541
 QY 622 ggggttgcacaaacttctgtcagcagcagcagcagcagcagcagcagcagcagcagcagc 681
 Db 542 GGGCCCTTCCAGCTTATAGGCAATAGATCCAGAAAGATAGACTTGTGAGAGAC 601
 QY 682 agactagaagtgatalttcaattctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 713
 Db 602 AAGCTGAAGGAGATGCTTCCGCTTCTTCCG 633
 RESULT 13
 LOCUS BF003501 635 bp mRNA EST 06-OCT-2000
 DEFINITION EST431999 KVI Medicago truncatula cDNA clone pKV1-7E15, mRNA
 ACCESSION BF003501
 VERSION BF003501.1 GI:10703776
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 635)
 Vandenbosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
 Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
 Fraser,C.M.
 ESTs from roots of Medicago truncatula 24 hours after inoculation
 with Sinorhizobium meliloti
 Unpublished (1999)
 Contact: Vandenbosch K
 Department of Biology
 Texas A&M University
 College Station, TX 77843-3258, USA
 Tel: 409 845 7707
 Fax: 409 845 2891
 Email: KateEmail.Bio.tamu.edu

Texas A&M University name: T267311e TIGR sequence name: MT1A032TK
 More information is available at: <http://chrysie.tamu.edu/medicago>
 Seq primer: SKmod (CTA gaa cta gta gaa cta cc).
 Location/Qualifiers
 1. 635
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"
 /clone="pKV1-7E15"
 /tissue="Seeding roots"
 /dev_stage="24 hours post-inoculation with Sinorhizobium
 meliloti"
 /lab_host="E. coli strain XL04R"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the Unizap XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-zap phage using Ex-assist
 helper phage and propagated in XL04R cells."

BASE COUNT 182 a 181 c 102 g 170 t
 ORIGIN
 Query Match 16.1%; Score 161; DB 11; Length 635;
 Best Local Similarity 56.9%; Pred. No. 3, 6e-36;
 Matches 336; Conservative 0; Mismatches 250; Indels 5; Gaps 2;

QY 244 gagaagcttctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 303
 Db 34 GACACAATCTCTCAGCAGCTATACCCCTTCACTGCTGTACCTCCTTATCTTGAANAAT 93
 QY 304 ttaagttccgtaactcctcccaactcttctcgaaaataccagaaagaatctcgcac 363
 Db 94 CTCGAATTCCCAACAACCTCCCAAGCTCAAGGCGCCCAATCAGCCCACTATCCGCAAGCTC 153
 QY 364 aaagacctaaatccctcagcagcagcagcagcagcagcagcagcagcagcagcagc 423
 Db 154 ACGAAGCTCAAGTATCTTTTCAATGAAATACCAACATGCTCAGGCGCCGATACCACTTTC 213
 QY 424 ttcctcagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 483
 Db 214 TTGCCCAAGCTTAAACACCTCCAGCTTCTTCACTTCCACCAACAACCTCAGGCCCG 273
 QY 484 atccctcctcagccttccactcttccgaaccttaagccctcagcagcagcagcagcagc 543
 Db 274 ATCCCAAGCTCACTTCTACAGCTACTTACCTTGAAGCTTACCTTACCTTACCTTACCT 313
 QY 544 ctcaacggtggaatcccgatatacttgggaatttgcctggatcccccgacatatac-- 601
 Db 334 CTCACAGGCCCAATTCAGAG-ATCATTCGCTTCTTCAAAAAGCCGCGCAATATATCAT 392
 QY 602 --tttcgatalaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 659
 Db 393 CTATATTCACACACCACTCTCTGCGCCATTCAGCTTATTAAGTCAATATATATCAATCA 452
 QY 660 taggcagcagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 719
 Db 453 AAGAAATAGACTTGTTCAGACAGCTTGAAGGAGATGCTGCTGCTTGTGGAAGGCCA 512
 QY 720 aaaagccttggaatctcagcagcagcagcagcagcagcagcagcagcagcagcagc 779
 Db 513 GAAGAAGACCAAAATCTGATGTTCTTGAAGAACTGTGTCTTTTGAATTTTCTAAGCT 572
 QY 780 gaagagcttccacccctcttgaacatactagcagcagcagcagcagcagcagcagcagc 830
 Db 573 TGATTTTCTTAACAGAGTTGATATGTTGATATTAATCAATACAGAT 623

RESULT 14
 LOCUS AV542271/C 587 bp mRNA EST 07-SEP-2000


```
OY 284 accatacactcccaagccttaigtgtccgtaaacctcccaatctttcggaanaatcc 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 274 ACCTTCATATCTCGAACAATTGGAAATTCATCATGTACTAATCTCACCGSACAATTC 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 344 cagaagaatcttcgcaactcaagaactlaaaatccctcagactcagctcagcagctca 403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 334 CACCTGCAATTCGGAAGCTCACAAATCTCAAAATGTTAAGCTCAGCTTCACTAACCTTA 393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 404 gtggccctgtcccttatcttcctcagactaagaaactaactgtttaagactatcgt 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 394 CAGGTCCGATCCCTGAATTCCTTAGTCAAGATTGACGTTGCTCGAGTTGAATT 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 464 ttaacaacttttggtgtaacccctccctcagcttccaccttccgaaacctlaagccc 523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 454 ACAATCAATTTACCGAACAATCCCTTCTTCCCTCTCAGCTTCGAAATTTGCTAGCGA 513
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OY 524 tgca 527
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DB 514 TGTA 517
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Search completed: March 13, 2002, 19:50:47
Job time: 4503 sec


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FT Modified-site 291..293
FT /label="N-glycosylation_site
FT /note="potential"
FT Peptide 25..49
FT /note="corresponds to CNBR peptide fragment which
FT was sequenced directly; the Cys residue at
FT position 27 could not be identified by
FT sequencing"
FT Peptide 215..246
FT /note="corresponds to CNBR peptide fragment which
FT was sequenced directly; the Ser residue at
FT position 232 and the Asn residue at
FT position 238 could not be identified by
FT sequencing"
PN USS5569830-A.
XX 29-OCT-1996.
XX
XX 03-MAY-1994; 94US-0238163.
XX
XX 03-MAY-1994; 94US-0238163.
XX
XX 03-MAY-1994; 94US-0238163.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Bennett A, Labavitch JM, Powell A, Stotz H;
XX WPI: 1996-496968/49.
XX DR N-PSDB: AAT49434.
XX
PT DNA construct, comprising poly:galacturonase inhibitor protein DNA
PT useful to confer resistance to fungal, partic. Botrytis cinerea,
PT infection in plant, pref. tomato or strawberry
XX
XX Claim 25; Fig 1; 33pp; English.
XX
CC The pear polygalacturonase inhibitor protein cDNA was obtained using
CC mRNA isolated from mature green fruit and the present amino acid
CC sequence was deduced from it. Pear PGIP exhibits differential
CC inhibition of polygalacturonases from different fungal species;
CC introduction of the pear PGIP cDNA into other plant species alters the
CC susceptibility of these plants to the fungal pathogens against which
CC pear PGIP is effective. For example, transgenic tomato fruit
CC expressing high levels of pear PGIP were shown to be more resistant
CC to the fungus Botrytis cinerea than control fruit.
XX
XX Sequence 330 AA:
SQ
Query Match 50.2%; Score 881.5; DB 17; Length 330;
Best Local Similarity 54.7%; Pred. No. 3.2e-82;
Matches 181; Conservative 41; Mismatches 106; Indels 3; Gaps 3;
OY 3 IESSEFCILICMFLCLPLNLSASORCANNNDKALLQIKTKAKRPRTTDSWSDDDCCGW 62
DB 1 melkfscflilclilfssvlnpalsdlonpdkkvlqikakfgpvyiaswksdtdcdw 60
OY 63 DLVECDENRRIISLIIODEALTGQIPQVGDLPYLOALFRRKLPNLFGRKIPRISALK 122
DB 61 yctcdettnrlnstlfaag-vsgqpalvagdpyletiefhknltgipipaklkl 119
OY 123 DLKSLRSLSTSLSGPVLPFPOLTKLTCLOLSEFKKLGAVIPOLSTLPNKLALHLENEL 182
DB 120 gllksrlstswlsgsvpdlfslqknlftlflstfnltgalpsiselpnlgalrldnkl 179
OY 183 TGEPLPQIFGNFAGS-PDIYSHNQLTGFPVKTFARADPRILDSGNGLEDDISFLRPPK 241
DB 180 tgnplstfggfignvpdiyslmqisnlpstsqmftstidstmklegdaasvltglnk 239
OY 242 RLEMLDFSGNVLSTFNSRQVFPSPSLYLDLNNQISGLSSELAKLDLOTFNVSNDMLC 301
DB 240 tctgvdslrnlllefnlskv-efpstsldvdmnkkiyslpvettqtnfqlnvsyrnlc 298

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OY 302 CKIPTGCLQRFDRATYLRHNSCLCGAPLPEC 332
DB 299 gqilpvggklqsfdeysyfhmrclcgaplpisc 329
RESULT 2
AAW09096
ID AAW09096 standard; Protein: 327 AA.
XX
XX AAW09096;
AC
XX
XX 05-MAR-1997 (first entry)
DI
XX
XX Tomato polygalacturonase inhibitor protein.
DE
XX
XX PGIP: polygalacturonase inhibitor protein; fungal resistance;
XX Botrytis cinerea; transgenic plant; tomato; strawberry.
XX
XX Lycopersicon esculentum.
OS
XX
XX USS5569830-A.
XX
XX 29-OCT-1996.
XX
XX 03-MAY-1994; 94US-0238163.
XX
XX 03-MAY-1994; 94US-0238163.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Bennett A, Labavitch JM, Powell A, Stotz H;
XX WPI: 1996-496968/49.
XX DR N-PSDB: AAT49435.
XX
PT DNA construct, comprising poly:galacturonase inhibitor protein DNA
PT useful to confer resistance to fungal, partic. Botrytis cinerea,
PT infection in plant, pref. tomato or strawberry
XX
XX Claim 26; Fig 2; 33pp; English.
XX
CC A fragment of tomato genomic DNA without introns and coding for
CC the polygalacturonase inhibitor protein was isolated from mature
CC green fruit. The DNA coding for PGIP can be introduced into of
CC plant species, e.g. strawberry, to alter the susceptibility of
CC these plants to the fungal pathogens against which tomato PGIP is
CC effective. The present PGIP amino acid sequence was deduced from
CC the genomic DNA; it includes a block of 10 tandem leucine-rich
CC repeats with an average length of 24 amino acids, as well as seven
CC potential N-glycosylation sites.
XX
XX Sequence 327 AA:
SQ
Query Match 48.1%; Score 844; DB 17; Length 327;
Best Local Similarity 52.8%; Pred. No. 2.3e-78;
Matches 171; Conservative 46; Mismatches 103; Indels 4; Gaps 3;
OY 11 LCICMFLCLPLNLSASORCANNNDKALLQIKTKAKRPRTTDSWSDDDCCGWLVCDE 70
DB 5 lllvllfclaspssivrcnpkdkvllqikdignpyhasvdpntdcdwywvllcdix 64
OY 71 SNRIISLIIODEALTGQIPQVGDLPYLOALFRRKLPNLFGRKIPRISALKSLRSL 130
DB 65 tnrlnalvfygan-issqipaavgdpyletiefhvnltltgipakltnlknrlis 123
OY 131 STSLSGPVLPFPOLTKLTCLOLSEFKKLGAVIPOLSTLPNKLALHLENELTGEPLDIF 190
DB 124 fnltgipidelfsqknlclllelnyngftgclipsisqipnllamyldrnklgtlpsf 183
OY 191 GNFAGS-PDIYSHNQLTGFPVKTFARADPRILDSGNGLEDDISFLRPPKRLMLDF 248
DB 184 grtkgpnlpdiylshnslgtnvpasigdlntfclstsrnklegdvsftgknktsqvldl 243

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PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159328.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	23-OCT-1999;	99US-0160989.
PR	23-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Db	7	1c1lfflfttclscldcngndkrtllkikkslnmphihsawdpqtccswylecgda	66
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Oy	130	SSTSISGVPLFPOLYTLTCLDLSFNKLGVIPQSLTLPNLKALHLEBELTGEIPDI	189
Db	127	swntltgplpdtfslglnkletfslsfnslspslsitpklialelsrnkltsipes	186
Oy	130	FGNFNGS-PDIYLSNLTGTVPKPFARADPRIDFSGNRLEGDISFLFGPKRLEMDF	248
Db	137	fsgfpgtvpdlrlshmgisgripkslgnidfntridlsrnklqgdasmfsgnktlwsidl	246
Oy	249	SGNVLSEFMSRVOEFPPLTYRLDLNHNQISLSLSESLAKLIDLQTFNVSNNLCKIPITGG	308
Db	247	srnmegfslsk-dtpkrlgldldhngltgtnipwqweaprlqfnnvsynklcghiprg	305
Oy	309	NLQRPDRATYLNHNSCLGAPLPEC	332
Db	306	kltfdisysyfnkclcgapleic	329
RESULT 4			
AAG46870			
ID	AAG46870 standard; Protein: 337 AA.		
XX	AAG46870;		
XX	18-OCT-2000 (first entry)		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 59012.		
XX	Protein identification: signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter		
XX	termination sequence.		
XX	Arabidopsis thaliana.		
XX	OS		
PN	EPI033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
XX			
PR	25-FEB-1999;	99US-0121825.	
PR	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
PR	23-MAR-1999;	99US-0125788.	
PR	25-MAR-1999;	99US-0126264.	
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DB 14 ICILCICFICLCISKIDCNQDKKILIKKSLINPYHLASWDPQTCSCWYCLECGDA 73
OY 70 TSNRIISLIIQDEDLTGQIPQVGDLPYLQALWFRKLPNLEGKPREISALKDLSRL 129
DB 74 LVNHVLTALISGQISGQIPAEVGDIPYLELTVFKLSNLGTLQPTAKIKNLMLTL 133
OY 130 SSTSLSGVPLEFFQILTKYLCIDLSFNKLGIVPPOLSTLPNKLALHLERNELTGEIPDI 189
DB 134 SWNLGTPIDTISQIKNLEFELSINDLSGSPSLSTLPKILALELSRNKLTGSIPES 193
OY 190 FGNFGCS-PDIYLSHNOITGVKPKFARADPRILDFSGNRLEGDISFLFGKKRLEMDP 248
DB 194 TGSIFGTVDPDIRLSHNGISGPIKSGINDIRIDLSRNKLQGDASMLGSGNKLTSIDL 253
OY 249 SGNVSEFNFSRVOEPPSLTYLDLHNQISGLSSESLAKLDLOEFNVSDNNLCGKIPFG 308
DB 254 SRMLGFGISKV-dIPKtLGldlnmgltgnlpqwcEarpqffnvsynkLcghlpvpg 312
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XX AAG07166;
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4215.
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hydrolisation assay: genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
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PD 06-SEP-2000. 1
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
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QY 70 TSN-RIISLIIODEALTGOIPPOVGDLPYLOALMFKKLEPNLEFGKIPPEISAKDLKSLR 128
DB 63 tvnhrvstllldgqe-issqilpeevglpyltstlffklntlgshdiphtaklknltfir 121

QY 129 LSTSTLSGPVPLFPPQTLKTLCTDLSFNKLLGVIPPOLSTLPNLIKALHLERNELTGCPD 168
DB 122 lswntltgvpweflsqklnleyldsfndisgsipselslrlkylelsrnkltgpipe 161

QY 189 IFGNFAGS-PDIYLSHQQLGFWPKTFARADPIRLDPSGMRLEGDISFLGPKRLEMLD 247
DB 182 stfgtsgkvpstflshmqstgltipksignpoflyridsrnkigqdasiltgakkltwivd 241

QY 248 FSGNVLSFNFSRYOEPPPSLTLYDLNHNQISGSLSSSLAKLDLOTENVSDNNLCGKIPTG 307
DB 242 isrnmgfdstkr-klaktlnmdmhngitgsipawskayqqlnvsvnrlogripkg 300

QY 308 GNLQREDRTAYLHNSCICGAPLPBC 332
DB 301 eylqridsystfhnkcicgaplpsc 325

RESULT 6
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AC AAG46832;
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58959.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PE 25-FEB-1999; 99US-0121825.
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PR 05-MAR-1999; 99US-0123180.
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PR 09-MAR-1999; 99US-0123548.
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PR 01-APR-1999; 99US-0127462.
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PR 01-JUN-1999; 99US-0137222.
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PR 10-JUN-1999; 99US-0138540.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Query Match 44.6%; Score 784; DB 21; Length 326;
Best Local Similarity 51.1%; Pred. No. 3.5e-72;

Matches 166; Conservative 45; Mismatches 104; Indels 10; Gaps 6;

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DB 3 ILLIILLITLTSakdclchddctllkikkslnpyhlaawbpktdccswylecgda 62
OY 70 TSN-RIISLITODEALTGQIPPOVGDLPYQALMFRLPNLFGKIPPEISALDKLSLR 128
DB 63 tvnhrveslilgdge-issqilpevgdipyltsllfkllthltghlptlaklnlclflr 121
OY 129 LSTSTLSGVPVLPFPQTLKTLCDLSFNKLGVIPOLSTLPNKLALHLERNELTGERTPD 188
DB 122 lswenltgvpelstqdklnleyldstfndlsqslssisslrlkleylslsrnkltgplpe 181
OY 189 IFGNFAGS-PIYISHNOJLGFVFKTFARADPIRLDFSGNRLEDDISFLGPKRLEMD 247
DB 182 stgltsgkvpstflshnglsqtlkslgnpdlfyridisrnltgqdaasllfyakktlwtvd 241
OY 248 FSGVNLSENFGRVOEPFPPSLTYLDLNNHNOISGSLSESLAKLIDLTFNVSDNNLCGKIPTG 307
DB 242 isrmfsgfdlskv-klaktlnldmhnngltgsipawskayfqllnvsyrnlcgrtlpkg 300
OY 308 GNLORFDRAYLHNSCUGAPLPFC 332
DB 301 eylgrfidsysffhncicgcaplpsc 325

RESULT 7

ID AAG07165 standard; Protein: 330 AA.

AC AAG07165;

DT -17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 4214.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX EPI033405-A2.
XX
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PD 06-SEP-2000.
XX
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 01-SEP-1999; 99US-0151930.

PR 07-SEP-1999; 99US-0152363.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 44.6%; Score 784; DB 21; Length 330;

Best Local Similarity 51.1%; Pred. No. 3; 6e-72;

Matches 166; Conservative 45; Mismatches 104; Indels 10; Gaps 6;

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QY 70 TSN-RIISLIODDEALGOTPOVGDLPYLOALWFRKLPMFLFKIPPEISALDKLSLR 128
DB 67 twnhtvstlllgdqe-issgqdpewgdipyltslfrlntlthgtpktlklknltflr 125
QY 129 LSTSLSGVPPLFPQTLKTLCLDSFNKLLGVIPPOQISTLPNKLALHLENNELTGEIPD 188
DB 126 lswntltgpyefltsqklnleyldstfndlspslsslrkleylslsnkltgpipe 185
QY 189 IFGNFAGS-PDIYUSHNOITGCFVFKTPARADPIRLDFSGNLEGDISTLFPPKRLKMLD 247
DB 186 sfgttslgkvpstflshnqslgtlpslgnpdyfrldstnrlqdasllfgakktwld 245
QY 248 FSGNVLSFNSFSGVOEFPPSLTYLDLNNHQISGSLSESLAKLDLOTFNVSNNLCGK1PTG 307
DB 246 lstrmfqfidskv-klaktlnlmdnmhngltslpaewskayfgllnvsynrlcgripkg 304
QY 308 GNLOFRRTAYLHNSCLGAPLPKC 332
DB 305 eylqfidsytsfhnkclcgaplpasc 329

RESULT 8
ACAG46831 standard; Protein; 330 AA.
ID ACAG46831;
AC ACAG46831;
XX
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 58958.
DE
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-030139.
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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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D b	7	I l l i l s t l l t s t a k e l o n c h d k t l l k l k s i m p y a s w d p r k d c c s w y c l e e g d a 66		
OY	70	T S N -R I I S L I I O D D E A L T G O I P P O V G U L P I Q A I M F F K L E N L E G K I P E E I S A L K D L K S R 128		
D b	67	t u n h v t s l l i q d g e -l s g q l p p e w g d p l y t l s t l i f k l i n l c g h a p t k a k n l t f l r 125		
OY	129	L S N S L S G P V L F F P O L K L L C L D L S E N K L G V I P P O L S T L P N L K A L H E R N E L T G E I P D 188		

Db	126	lswnltpvpbeflssqklnleyldistfindisgslpsisslrlrkeylelsrnkltpipe	185
Oy	169	IFGNAGS-PIYVLSHNOITGCFVPTFEARADPIRLDPSGNRLEGDISFLPGPKRLEMLD	247
Db	166	sfgtsgkvpasflshmqslsgtlpkslgnpdlfyridlsrnklgdsallfgakktwlvd	245
Oy	248	FGSNVLSTNFSRVOEFPPSLTYLDLNNQISGSLSELAKLDLOTFNVSDDNNLCGIPTG	307
Db	246	lsrmfqlslskv-klaktlnlmdnmhngltgsipaewskayfqllnvsyrrlrgripkg	304
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DT	18-OCT-2000	(first entry)	
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DE	Protein identification: signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter		
KW	termination sequence.		
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OY 189 IFGNFAGS-PDIYLSHNOITGVFKTFARADPIRLDFSGNRLEGDISFLFGPKRLEMD 247
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OY 248 FSGNVLSFNSRVOEPPLTYLIDLNNHOISGSLSELAKLDLQTFNVSDDNLCGRIPMG 307
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RESULT 10
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XX AC AAG07164;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 4213.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

XX PN EPI033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX XX 25-FEB-1999; 99US-0121825.

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Best Local Similarity 49.7%; Pred. No. 1.1e-71;
Matches 160; Conservative 44; Mismatches 115; Indels 3; Gaps 3;

QY 13 ICMIFLCLPMLASQRCNNNDKQALLQIKALKPPTITDSWSDCCGMDVBC-DETS 71
DB 18 lllflftlclskdlnqndkllikkslnmpylaswdpqtdccsyclecgdatv 77
QY 72 NRTISLIQDDEALTGOIPQVGDPLVLOALWPKRLPNLFGKIPEETISALKDKSLRSS 131
DB 78 nhrvtaltltsqslsgslpaevgdlpylectivtkisnlcglqptlaktknltmrlfsw 137
QY 132 TSLSGPYLPFPOLTKLTLCDLSFNKLLGVIPOLSTLPNKLALHERNELTGEIPDFG 191
DB 138 tnlgtlpdftlsqknlleflelndslsgslpslslclpkllalelslmnltslpsfsg 197
QY 192 NFAGS-PDITLSHNOITGVPKTFARADPIRLDFSGNRLEGDISLFLGPKKRLMDLDFG 250
DB 198 sfpgtyvpdlrlnmqslsgslpkslgnldfnrlidstrnlklsqdasmlfgsnkktwsldslr 257
QY 251 NVLSFNFSRVQEPSPSLTYDLNHNQISGSLSEFLAKLDQTFNVSDNNCGKITPGGNL 310
DB 258 nmfgdlslkv-dlplktlglldlnmgltglnlpvwteaplfqfnvsnkclgnhpggkl 316
QY 311 QRPDRAYLVHNSCLGAPLPEC 332
DB 317 qtfdsysyfnkclcgaplelc 338

RESULT 13
AAG23196
ID AAG23196 standard; Protein; 325 AA.
XX
AC AAG23196;
XX

DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26412.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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Best Local Similarity 47.2%; Pred. No. 1.9e-65;
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QY 74 IISLIQDDEALTGQIPPOVDLPYLQALMFKRLPNLFGKIPFEISALDLSRLSTS 133
DB 68 VGLSVLTSGE-VSGQSYIGLVDLRTLDISYLPHTLGNPRTIKLKNLNTLYKHSS 126
QY 134 LSGPVLPFFPOLTKLCLDLSFNKLGIVPPOLSTIPNLKALHLERNELTGEIPDIFGNF 193
DB 127 LSGPILPDYISELKLFIIDISINQFTGPIGPSLSQMPKLEAQINDKNKLTSGISNFSGF 186
QY 194 ACS-PDIYSHNOQLTFVFKTFARADPIRLDFSGNRLDEGDISFLGPKRRLKLEMLDFSGNV 252
DB 187 VGNVPLIYSNMKLSKIPESISKYDFNAVDLSNGFEGDAFMIFGRNKTCTVRVDLSIRM 246
QY 253 LSFNFSGVGEFPPSLTYLDLNNHQISGSLSSSELAKLQDTFNVSDNNLCKIPTGCGNLR 312

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DB 247 fntdlkv-kfarsivldisqnhlygkipalclklnlhnfnvsdnhlgcklpsgllt 305
QY 313 FDRATVLIHNSCLCGAPLPEC 332
DB 306 fepsafehniclcpkac 325

RESULT 14
AAR37817
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AC AAR37817;
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DT 01-OCT-1993 (first entry)
DE Sequence of fungine endopolylgalacturonase inhibitor (PGIP).
XX
KW Fungine endopolylgalacturonase inhibitor (PGIP); PCR; primer;
XX pesticide.
XX
OS Phaseolus vulgaris, strain Saxa.
XX
PN WO9311241-A.
XX
PD 10-JUN-1993.
XX
PF 04-DEC-1992; 92WO-IT00158.
XX
PR 06-DEC-1991; 91IT-ORM0915.
XX
PA (CNDR ) CONSIGLIO NAZ DELLE RICERCHE.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI Albersheim P, Bergmann C, Cervone F, Darvill A;
PI De Lorenzo G, Salvi G;
XX
DR WPI: 1993-197059/24.
DR N-PSDB: AA042595.
XX
PT Nucleotide sequence contained in recombinant vector - encodes
PT endo-polygalacturonase inhibitor (PGIP), useful for conferring
XX e.g. fungal resistance to plants
XX
PS Claim 16; Page 18-19; 36pp; English.
XX
CC The PGIP is capable of inhibiting activity of the fungine
CC endo-alpha-1,4-D-poly-galacturonase enzyme (PG). PGIP is useful
CC in plant transformation to confer fungal resistance or resistance
CC to micrororganisms pathogenicity.
XX
SQ Sequence 342 AA:

```

```

Query Match          35.4%; Score 622; DB 14; Length 342;
Best Local Similarity 41.0%; Pred. No. 1.8e-55;
Matches 141; Conservative 56; Mismatches 127; Indels 20; Gaps 7;

QY 2 NIESSEPCILICIMFLCPNLSASQRCNNNDKQALLQIKTALKNPTITDSWVSDDDCG 61
DB 5 nlpvmsassllilvlalrelalselcnpqgqallqkkdignptltswwipitdcn 64
QY 62 --WDVCECETSN--RIISLIQDDEALTGQ-----IPPOVDLPYLQALMFKRLPN 110
DB 65 rtwlgvldctdcqyrvnvl-----disghmlpkypipssianlpynlfiyiggnl 118
QY 111 FCKIPEEISALDLSRLSTSLSGVPPLFPOLTKLCLDLSFNKLGIVPPOLSTIP 170
DB 119 vgpilpalaklqlylylthcnvsgalpdflsqiklvtldfsynaigqlppsisip 178
QY 171 NUKALHLERNELTGEIPDIFGNFAG-SPDIYSHNOQLTFVFKTFARADPIRLDFSGNRL 229
DB 179 nlgaltfdgnrtisgaipdeygsfskfltamltisrnlcgkippftanlnlafvdlsrml 238

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2002, 20:14:09 ; Search time 22.58 Seconds

(without alignments)
330,872 Million cell updates/sec

Title: US-09-308-140-7

Perfect score: 1756

Sequence: 1 MNISSECPILICMIFLCL.....FDRATVHLNSCLCAPLPEC 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	881.5	50.2	330	1	US-08-238-163-2
2	844	48.1	327	1	US-08-238-163-4
3	632	35.4	342	1	US-08-244-646-15
4	622	35.4	342	1	US-08-592-9368-21
5	464.5	26.5	227	1	US-09-111-573-21
6	322.5	18.4	968	4	US-08-244-646-17
7	320.5	18.3	968	4	US-09-180-439-4
8	319.5	18.2	1016	4	US-09-180-439-3
9	315.5	18.0	1196	4	US-09-180-439-8
10	315.5	18.0	1196	4	US-08-881-706-2
11	315	17.9	1112	4	US-09-353-585-2
12	315	17.9	1112	4	US-09-353-585-3
13	311.5	17.7	999	4	US-08-473-553A-5
14	300.5	17.1	799	4	US-09-180-439-6
15	300.5	17.1	1012	2	US-08-475-891A-4
16	300.5	17.1	1025	2	US-08-567-375-4
17	300.5	17.1	1025	2	US-08-587-680A-4
18	283	16.1	863	4	US-08-666-271-2
19	278.5	15.9	863	4	US-08-945-983-2
20	273	15.5	980	2	US-08-473-553A-5
21	273	15.5	985	2	US-08-473-553A-2
22	264	15.0	523	2	US-08-473-553A-3
23	226.5	12.9	1023	2	US-08-475-891A-2
24	226.5	12.9	1023	2	US-08-567-375-2
25	226.5	12.9	1023	2	US-08-587-680A-2
26	188	10.7	268	4	US-09-353-585-6
27	172	9.8	301	4	US-09-353-585-5

28	172	9.8	544	2	US-08-587-680A-25	Sequence 25, Appl
29	155	8.8	277	2	US-08-567-375-16	Sequence 16, Appl
30	154.5	8.8	375	1	US-08-303-238-2	Sequence 2, Appl
31	154.5	8.8	375	4	US-08-458-834-2	Sequence 2, Appl
32	149.5	8.5	605	4	US-09-063-950-5	Sequence 5, Appl
33	147	8.4	282	1	US-08-442-063A-45	Sequence 45, Appl
34	147	8.4	307	1	US-08-442-063A-48	Sequence 48, Appl
35	147	8.4	333	1	US-08-442-063A-27	Sequence 27, Appl
36	147	8.4	342	1	US-08-672-919-2	Sequence 2, Appl
37	147	8.4	342	1	US-08-619-916-2	Sequence 2, Appl
38	147	8.4	342	5	PCT-US95-08542-2	Sequence 2, Appl
39	147	8.4	359	1	US-08-303-238-4	Sequence 4, Appl
40	147	8.4	359	4	US-08-458-834-4	Sequence 4, Appl
41	146.5	8.3	605	1	US-08-190-802A-49	Sequence 49, Appl
42	146.5	8.3	605	4	US-08-477-346-49	Sequence 49, Appl
43	146	8.3	376	1	US-08-303-238-1	Sequence 1, Appl
44	146	8.3	376	4	US-08-458-834-1	Sequence 1, Appl
45	144.5	8.2	603	1	US-08-190-802A-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-238-163-2
Sequence 2, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: FOWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-238-163-2

Query Match 50.2%, Score 881.5, DB 1, Length 330,
Best Local Similarity 54.7%, Pred. No. 7,1e+88;
Matches 181; Conservative 41; Mismatches 106; Indels 3; Gaps 3;
QY 3 ISSSECPILICMIFLCLPNLSASORCNNDKALQIKTKALNPTITDSDWSDDCGGM 62

Query Match 35.4%; Score 622; DB 1; Length 342;

Best Local Similarity 41.0%; Pred. No. 1.5e-59; Indels 20; Gaps 7;

Matches 141; Conservative 56; Mismatches 127;

QY 2 NISSFCPLICMIFLCIPNLASORCNNDKQALLQIKTKALNPTTIDSWSDDCG 61
 DB 5 NIPVMSSSLITLVLSRTALSELCPQKQALLQIKTKALNPTTIDSWSDDCG 64
 QY 62 --WDVECOETSN--RIISLIIDDEALTGQ-----IPQVGDLPYQALMFKRLPL 110
 DB 65 RTWGLVLCPTDQTYRVNML-----DLGHNLPKPYIPSSLANPYLNFLYIGGINNL 118
 QY 111 FCKIPEISALDKLSRLSTSLSGPVLPFPOLTKLCLDLSEFKLGLVLPOLSTLP 170
 DB 119 VGPPIPAIAKLQHLHYLTHTNVSGAIPDLSQIKTLVTLDFSYNALSGTLPPSISLP 178
 QY 171 NUKALHERNELTGEIPDIFGNFAG--SPDIYLSHNOITGEVPEKTFARADPIRLDFSGNRL 229
 DB 179 NLGITFDGNRISGAIPDSYGSFKLTAMTISRNLTKIPPTFANLMAFVDSLRLML 238
 QY 230 EGDISFLGPKKRLKLEMDPSGNVLSFNSRVOEPPSLTYLDLNNQISGLSSELAKLD 289
 DB 239 EGDASVLFSGDKTKIKHLAKNSLAFDLGKV--GLSKNLGLDLRNNRIYGTLPQGLTOLK 297
 QY 290 -LOTFNVSNNLCGRIPGTGNLQRPDRTAYLHNSCLCGAPLPEC 332
 DB 298 FLOSLNVSFNNLCGEIPQGNLKRFDVSSYANNKCLCGSPLPSC 341

RESULT 4

US-08-592-936B-21

; Sequence 21, Application US/08592936B

; Patent No. 5783393

; GENERAL INFORMATION:

; APPLICANT: Kelllogg, Jill A.

; TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS: REGULATED EXPRESSION OF TRANSGENES IN PLANTS

; ADDRESS: Dehlinger & Associates

; STREET: 350 Cambridge Avenue, Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/592,936B

; FILING DATE: 29-JAN-1996

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Evans, Susan T.

; REGISTRATION NUMBER: 38,443

; REFERENCE/DOCKET NUMBER: 4257-0012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 324-0880

; TELEFAX: (650) 324-0960

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 342 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHEICAL: NO

; ORIGINAL SOURCE: predicted amino acid coding sequence

INDIVIDUAL ISOLATE: of SEQ ID NO:20

US-08-592-936B-21

Query Match 35.4%; Score 622; DB 1; Length 342;

Best Local Similarity 41.0%; Pred. No. 1.5e-59; Indels 20; Gaps 7;

Matches 141; Conservative 56; Mismatches 127;

QY 2 NISSFCPLICMIFLCIPNLASORCNNDKQALLQIKTKALNPTTIDSWSDDCG 61
 DB 5 NIPVMSSSLITLVLSRTALSELCPQKQALLQIKTKALNPTTIDSWSDDCG 64
 QY 62 --WDVECOETSN--RIISLIIDDEALTGQ-----IPQVGDLPYQALMFKRLPL 110
 DB 65 RTWGLVLCPTDQTYRVNML-----DLGHNLPKPYIPSSLANPYLNFLYIGGINNL 118
 QY 111 FCKIPEISALDKLSRLSTSLSGPVLPFPOLTKLCLDLSEFKLGLVLPOLSTLP 170
 DB 119 VGPPIPAIAKLQHLHYLTHTNVSGAIPDLSQIKTLVTLDFSYNALSGTLPPSISLP 178
 QY 171 NUKALHERNELTGEIPDIFGNFAG--SPDIYLSHNOITGEVPEKTFARADPIRLDFSGNRL 229
 DB 179 NLGITFDGNRISGAIPDSYGSFKLTAMTISRNLTKIPPTFANLMAFVDSLRLML 238
 QY 230 EGDISFLGPKKRLKLEMDPSGNVLSFNSRVOEPPSLTYLDLNNQISGLSSELAKLD 289
 DB 239 EGDASVLFSGDKTKIKHLAKNSLAFDLGKV--GLSKNLGLDLRNNRIYGTLPQGLTOLK 297
 QY 290 -LOTFNVSNNLCGRIPGTGNLQRPDRTAYLHNSCLCGAPLPEC 332
 DB 298 FLOSLNVSFNNLCGEIPQGNLKRFDVSSYANNKCLCGSPLPSC 341

RESULT 5

US-09-111-573-21

; Sequence 21, Application US/09111573

; Patent No. 5929302

; GENERAL INFORMATION:

; APPLICANT: Kelllogg, Jill A.

; TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS: REGULATED EXPRESSION OF TRANSGENES IN PLANTS

; ADDRESS: Dehlinger & Associates

; STREET: 350 Cambridge Avenue, Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/111,573

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/592,936

; FILING DATE: 29-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Evans, Susan T.

; REGISTRATION NUMBER: 38,443

; REFERENCE/DOCKET NUMBER: 4257-0012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 324-0880

; TELEFAX: (650) 324-0960

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 342 amino acids

; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: predicted amino acid coding sequence
INDIVIDUAL ISOLATE: of SEQ ID NO:20
US-09-111-573-21

Query Match 35.4%; Score 622; DB 2; Length 342;
Best Local Similarity 41.0%; Pred. No. 1.5e-59;
Matches 141; Conservative 56; Mismatches 127; Indels 20; Gaps 7;

Db 2 NIESSFCPIICMIFLCLPNLSASQRCNNNDKQALLQIKALKNPITTDSDVSDDDCC 61
5 NIPVWSSSLTIVLVSRLTALSCLNPDQKALLQIKDLGPTLLSSWLPPTDDCN 64
62 --WDLVECDSTN--RIISLIIDDEALTGO-----IPQVGDLPYLQALMFRKLPNL 110
65 RTWGLVLCDTQGTQRYVNL-----DLSGHNLPKRYPIPSLALPLNLYIGGINNL 118
111 FGKIPPEISALKDLKSLRSLSTSLSGVPVLPFPQTLTKLCLDLSEFNKLLGYIPOLSTLP 170
119 VGPPIPAIAKLTQLHYLYITHTNWSGAIPDFLSQIKTLVTLDFSYNALSGTLPPSISLP 178
171 NLKALHLERNELTGEIPDIFGNFAG--SPDIYLSHNQLTGFVFKTFARADPIRLDSSGNRL 229
179 NLGGTFEGNRIISGIIIPDSYGSFKLFTAMTISRRLTKIPPTFANLNLAFFVDSLRL 238
230 EGDISFLFGPKRLEMLDFSGNVLSFNFSRVQEPFPLTYLDLNHNOISGSLSELAKLD 289
239 EGDASVFLGSDKNTKIKILAKNSLAFDLGV--GLSKNLNGDLRNNRITGTLPGQTLQ 297
290 -LQFTNVSNNLCKIPTGNNLQRPDRTAYLHNSCLGAPLPEC 332
298 FLQSLNVSFNNLCEIPQGNLKRFDVSSYANNKCLCGSPLPSC 341

RESULT 6
US-08-244-646-17
Sequence 17, Application US/08244646
Patent No. 5744692
GENERAL INFORMATION:
APPLICANT: Cervone, Felice
APPLICANT: De Lorenzo, Giulia
APPLICANT: Salvi, Giovanni
APPLICANT: Albersheim, Peter
APPLICANT: Darvill, Alan
APPLICANT: Bergmann, Carl
TITLE OF INVENTION: Nucleotide Sequences Coding An
TITLE OF INVENTION: Endopolygalacturonase Inhibitor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sally A. Sullivan
STREET: 5370 Manhattan Circle Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,646
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 91A 000915
FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/IT/00158

FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 19-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-244-646-17

Query Match 26.5%; Score 464.5; DB 1; Length 227;
Best Local Similarity 43.4%; Pred. No. 1.2e-42;
Matches 98; Conservative 41; Mismatches 84; Indels 3; Gaps 3;

Db 109 NLFKIPPEISALKDLKSLRSLSTSLSGVPVLPFPQTLTKLCLDLSEFNKLLGYIPOLST 168
2 NLVGPPIPAIAKLTQLHYLYITHTNWSGAIPDFLSQIKTLVTLDFSYNALSGTLPPSISLP 61
169 LPNKALHLERNELTGEIPDIFGNFAG--SPDIYLSHNQLTGFVFKTFARADPIRLDSSGN 227
62 LPNVIGTFEGNRIISGIIIPDSYGSFKLFTAMTISRRLTKIPPTFANLNLAFFVDSLRL 121
228 RLEDISFLFGPKRLEMLDFSGNVLSFNFSRVQEPFPLTYLDLNHNOISGSLSELAKLD 287
122 MLDGDSVFLGSDKNTKIKILAKNSLAFDLGV--GLSKNLNGDLRNNRITGTLPGQTLQ 180
288 LD-LQFTNVSNNLCKIPTGNNLQRPDRTAYLHNSCLGAPLPEC 332
181 LKPLHSLNVSFNNLCEIPQGNLQTFHVSAYANNKCLCGSPLPAC 226

RESULT 7
US-09-180-439-4
Sequence 4, Application US/09180439
Patent No. 6225532
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
APPLICANT: Hatzixanthis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
FILE REFERENCE: 620 -53
CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
EARLIER APPLICATION NUMBER: GB 9619924.5
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 968
TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-09-180-439-4

Query Match 18.4%; Score 322.5; DB 4; Length 968;
Best Local Similarity 29.3%; Pred. No. 3.8e-26;
Matches 111; Conservative 45; Mismatches 142; Indels 81; Gaps 12;
Db 30 NNNDKQALLQIKALKNP--TITDSWVSDDDC--GMDLVSC----- 67
27 STEATALLWKATFFKNQNSFLASWTTSSNACKDYGVCVCLNGRVNTLITNASVIGTL 86

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QY 68 -----DETSNRI-----ISLIID--DEALGOIPPOVDLPYQ 100
DB 87 YAFPFSSLPFLENLDLNNISGTTIPEIGNLNLVLDLNTNOISGTTIPQIGSLAKIQ 146
QY 101 ALMFRKLPN-LFGKIPPEISALKDKLSRLSSTLSGVPVLPFPOLTKLTCGLDSFKKL 159
DB 147 II--RIFNNHLNGFIPEEIGYLRSLTKLSLGINFLSGSIPASIGNMTLSFLYENOLS 204
QY 160 GVIPPOLSTLPNKLALHERNELTGEIPDIFGNFAGSPDIYLSHNOITGVPKTFARADP 219
DB 205 GFIPPEIGYLRSLTKLSLGINFLSGSIPASIGNMTLSFLYENOLS 264
QY 220 I-RDPSGNRLEGGDISFLGPKRKREMLDFSGNVLSFNSRVOEFPPLSTYLDLNNHOIS 278
DB 265 LTKLSLGINFLSGSIPASIGNMTLSRLDLVNNKLSGSIPEEIGYLRSLTYLDLGENALN 324
QY 279 GSLSSELAKL-DLQTFVSDNNLCGKIP-----TGGNLOR 312
DB 325 GSIPSSLGNNLNSRLDLVNNKLSGSIPEEIGYLRSLTYLDLGENALNSIPASIGNLNN 384
QY 313 FDRATYLNHNSCAGAPLPE 331
DB 385 L-FMLYLYNNOLSGS-IPE 401

RESULT 8
US-09-180-439-3
; Sequence 3, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; APPLICANT: Jones, Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; FILE REFERENCE: 620 - 53
; CURRENT APPLICATION NUMBER: US/09/180,439
; EARLIER FILING DATE: 1998-12-06
; EARLIER APPLICATION NUMBER: PCT/GB97/01249
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: GB 9609681.3
; EARLIER FILING DATE: 1996-05-09
; EARLIER APPLICATION NUMBER: GB 9619924.5
; EARLIER FILING DATE: 1996-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-180-439-3

Query Match 18.3%; Score 320.5; DB 4; Length 968;
Best Local Similarity 29.3%; Pred. No. 6,2e-26;
Matches 111; Conservative 44; Mismatches 143; Indels 81; Gaps 12;

QY 30 NNNKQALLQIKTALKNP--TITDSWVSDDCC-GMDLVEG----- 67
DB 27 STEBATALLKWKATFKKQNNNSFLASWTSSNACKDWYGVCLNGRVNTLNTNASVIGTL 86
QY 68 -----DETSNRI-----ISLIID--DEALGOIPPOVDLPYQ 100
DB 87 YAFPFSSLPFLENLDLNNISGTTIPEIGNLNLVLDLNTNOISGTTIPQIGSLAKIQ 146
QY 101 ALMFRKLPN-LFGKIPPEISALKDKLSRLSSTLSGVPVLPFPOLTKLTCGLDSFKKL 159
DB 147 II--RIFNNHLNGFIPEEIGYLRSLTKLSLGINFLSGSIPASIGNMTLSFLYENOLS 204
QY 160 GVIPPOLSTLPNKLALHERNELTGEIPDIFGNFAGSPDIYLSHNOITGVPKTFARADP 219
DB 205 GFIPPEIGYLRSLTKLSLGINFLSGSIPASIGNMTLSFLYENOLS 264
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QY 220 I-RDPSGNRLEGGDISFLGPKRKREMLDFSGNVLSFNSRVOEFPPLSTYLDLNNHOIS 278
DB 265 LTKLSLGINFLSGSIPASIGNMTLSRLDLVNNKLSGSIPEEIGYLRSLTYLDLGENALN 324
QY 279 GSLSSELAKL-DLQTFVSDNNLCGKIP-----TGGNLOR 312
DB 325 GSIPSSLGNNLNSRLDLVNNKLSGSIPEEIGYLRSLTYLDLGENALNSIPASIGNLNN 384
QY 313 FDRATYLNHNSCAGAPLPE 331
DB 385 L-FMLYLYNNOLSGS-IPE 401

RESULT 9
US-09-180-439-8
; Sequence 8, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; APPLICANT: Jones, Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; FILE REFERENCE: 620 - 53
; CURRENT APPLICATION NUMBER: US/09/180,439
; EARLIER FILING DATE: 1998-12-06
; EARLIER APPLICATION NUMBER: PCT/GB97/01249
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: GB 9609681.3
; EARLIER FILING DATE: 1996-05-09
; EARLIER APPLICATION NUMBER: GB 9619924.5
; EARLIER FILING DATE: 1996-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1016
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-180-439-8

Query Match 18.2%; Score 319.5; DB 4; Length 1016;
Best Local Similarity 29.0%; Pred. No. 8,6e-26;
Matches 110; Conservative 45; Mismatches 143; Indels 81; Gaps 12;

QY 30 NNNKQALLQIKTALKNP--TITDSWVSDDCC-GMDLVEG----- 67
DB 27 STEBATALLKWKATFKKQNNNSFLASWTSSNACKDWYGVCLNGRVNTLNTNASVIGTL 86
QY 68 -----DETSNRI-----ISLIID--DEALGOIPPOVDLPYQ 100
DB 87 YAFPFSSLPFLENLDLNNISGTTIPEIGNLNLVLDLNTNOISGTTIPQIGSLAKIQ 146
QY 101 ALMFRKLPN-LFGKIPPEISALKDKLSRLSSTLSGVPVLPFPOLTKLTCGLDSFKKL 159
DB 147 II--RIFNNHLNGFIPEEIGYLRSLTKLSLGINFLSGSIPASIGNMTLSFLYENOLS 204
QY 160 GVIPPOLSTLPNKLALHERNELTGEIPDIFGNFAGSPDIYLSHNOITGVPKTFARADP 219
DB 205 GFIPPEIGYLRSLTKLSLGINFLSGSIPASIGNMTLSFLYENOLS 264
QY 220 I-RDPSGNRLEGGDISFLGPKRKREMLDFSGNVLSFNSRVOEFPPLSTYLDLNNHOIS 278
DB 265 LTKLSLGINFLSGSIPASIGNMTLSRLDLVNNKLSGSIPEEIGYLRSLTYLDLGENALN 324
QY 279 GSLSSELAKL-DLQTFVSDNNLCGKIP-----TGGNLOR 312
DB 325 GSIPSSLGNNLNSRLDLVNNKLSGSIPEEIGYLRSLTYLDLGENALNSIPASIGNLNN 384
QY 313 FDRATYLNHNSCAGAPLPE 331
DB 385 LSRDL-LVNNKLSGS-IPE 401
```


RESULT 10
US-08-881-706-2
Sequence 2, Application US/08881706
Patent No. 6245969
GENERAL INFORMATION:
APPLICANT: Chong, Joane
APPLICANT: Li, Jianming
TITLE OF INVENTION: Receptor Kinase BIN1
FILE REFERENCE: 07251/022001
CURRENT APPLICATION NUMBER: US/08/881,706
CURRENT FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1196
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-08-881-706-2

Query Match 18.0%; Score 315.5; DB 4; Length 1196;
Best Local Similarity 28.3%; Pred. No. 3.1e-25;
Matches 112; Conservative 48; Mismatches 143; Indels 93; Gaps 13;

QY 20 LPTNSAS-----QRCNNNDKQALLQIKALKNP--TITDSWVSDDCCGW--DLVECDT 70
DB 385 LTNLSASLRLTLSSNFGSPIL--PMLCONPKNTLOELTLQNNFTGKIPPTLSNCSE- 441
QY 71 SNRIISLIIDDEALTGPVQDLPYLO--ALMFRKLPLNFGKIPPEISALKDLKSLR 128
DB 442 ---LVSLHLSEFN-VLSGTITSSLSGLSKLDKMLMLE---GEIQELMYVKTETLI 494
QY 129 LSSTSLSGPVLPFPQTLKTCLDLSFNKLLGVIPQLSTPLNKAHLERNELTGEIPD 188
DB 495 LDFNDLTGEIPSGISLNTNLMWISLNNRLTGEIPKWIGRLNLAIKLSNNSGSIIPD 554
QY 189 IFGNFASPIIYLSHNLGTGFVPT--FARADPTLDF-----SGN 227
DB 555 ELGGCRSLMLDLNTLNTNGTIPAMFGQSGKIAANFIAGRRVYIKNDMKKECHGAGN 614
QY 228 RLE-----DISPLFGPKRLEMLDFSGVLSFNSRVQ 261
DB 615 LLEFGIRSDQLANLSTRNCNITSRYVGHSTPTFDNNSMFLDMSTYMLSGYIKETI 674
QY 262 EFPPLTYLDLNNQISLSSELA-----KLD-----LOTFNVS 296
DB 675 GSNPYLFLNMGHNDISGIPDEVGLRGILNILDLSNKLGDRIPOAMSA/LTMLTEIDLS 734
QY 297 DNNLCGKIPTGCGNQRDRATAYLHNSCLGAPLPEC 332
DB 735 NNNLSGPIPEMGOFETFPAPKFLNNGLCGYPPLRC 770

RESULT 11
US-09-353-585-2
Sequence 2, Application US/09353585
Patent No. 6287865
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12O 1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 950658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-353-585-2

Query Match 17.9%; Score 315; DB 4; Length 1112;
Best Local Similarity 30.8%; Pred. No. 3.1e-25;
Matches 108; Conservative 41; Mismatches 146; Indels 56; Gaps 11;

QY 30 NNNDKQALLQIKALKNP--TITDSWV--SDDCCGWDVLEC----- 67
DB 27 STEEATALLKMKATFFKNNNSFLASWIPSSNACKDWYGVVCFNGRVNTLNTASVIGTL 86
QY 68 -----DETSNRI-----ISLIID--DEALTGOIIPVQDLPYLO 100
DB 87 YAFPPSSLPSEMLDLSKNNIYGTIPPEIGNLTNLVYLDLNNQISGTLIPQIGLAKID 146
QY 101 ALMFRKLPLN-LFGKIPPEISALKDLKSLRSLSTSLSGPVLPFPQTLKTCLDLSFNKLL 159
DB 147 II--RIFHQNLNGFIPEKIGYLRSLTKLSLGINFLSGSI PASVGNLNNLSFLYLYNNQLS 204
QY 160 GVIPQLSTPLNKAHLERNELTGEIPDFGNFASPIIYLSHNLGTGFVPTFARAPD 219
DB 205 GSIPPEIYLRSLTELDLSDNALNGSIPASLGMMNLSFLYGNQLSGSIPPEICYLRS 264
QY 220 IR-LDFSGNRLEGGISFLFGPKRLEMLDFSGVLSFNSRVQEFPPSGTYLDLNNQIS 278
DB 265 LTYLDLSENALNGSIPASGNNLNSFLYGNQLSGSIPPEICYLRS/LNVLGSLSEMAIN 324
QY 279 GSLSSEFLAKV-LDLOTFNVSDNNLCGKIPTG--GNLQRFDRATAYLHNSCLGCA 327
DB 325 GSIPASIGNLKLSRLNLVNNQLSGSIPASLGTLNLS--MLYLYNNQLSGS 374

RESULT 12
US-09-353-585-3
Sequence 3, Application US/09353585
Patent No. 6287865
GENERAL INFORMATION:

```

APPLICANT: Dixon, Mark S
            Jones, David A
            Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12O
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/G896/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-353-585-3

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```

Query Match 17.9%; Score 315; DB 4; Length 1112;
Best Local Similarity 30.8%; Pred. No. 3.1e-25;
Matches 108; Conservative 41; Mismatches 146; Indels 56; Gaps 11;
30 NNNDKALLQITALKNP--TTDSWV-SDDCCGMDLVECC----- 67
27 STEEATALLKMKATEFNQNSFLASWIPSSNACKOWYGVCFGRVNTLNTNASVIGTL 86
68 -----DETSRI-----ISLIID--DEALTGOIPPOVGDLPYQ 100
87 YAFPPSSLPSELENLDSKNINIGTIPPEIGNLTLNLYLDLNNNOISGTIPQIGLAKIQ 146
101 ALMFKLPN-LFGKIPPEISALKDKLSRLSTSLGVP/LFFPOLTKTCDISFNKTL 159
147 IL--RIFHNQNLGFIPEKELGYRLSLKLSLGINFLSGSIPASVGNLNNLSFLYLYNNQLS 204
160 GYIPPOLSTPLMKLHLERNELTGEIPDIFGNFAGSPDIYLSHNLGTGFVKTPARADP 219
205 GSIPPEISYLSRLTELDSDNALNGSIPASLNMNNLSFLFLYGNLGSIPPEELCYLRS 264
220 IR-LDFSGRLGSDISLFGPKKRLKLEMDFSGNVLSFNFSSRVOEPPSLTYLDLNNHOIS 278

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Db 265 LTYLDLSENALNGSIPASIGNLNLSFLFLYGNLGSIPPEIGYRLSLNVLGSEMLN 324
OY 279 GSLSELKKL-DLQFNYSNDNLCKIPTG--GNLQRFDTAYLAHSCICGA 327
Db 325 GSIPASLGNLKLRLNLVNNQSLGSIPASIGNLNLS-MLYLYNNQSLGS 374

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RESULT 13
US-08-473-553A-5
Sequence 5, Application US/08473553A
Patent No. 5859338
GENERAL INFORMATION:
APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 999 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-473-553A-5

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Query Match 17.7%; Score 311.5; DB 2; Length 999;
Best Local Similarity 26.6%; Pred. No. 6.3e-25;
Matches 115; Conservative 49; Mismatches 125; Indels 143; Gaps 16;
7 FCPILICIFLCPLNLSAQRNNNDKQALLQITALKNPIT--DSWVSDDC--CGWD 63
3 YCLILCLLSYLLPSLSL--NODATILRQAKLGSDPAQSLSSWSDNNNDYTPCKKL 57
64 LVECDETS-----RIL 75
58 GVSQATSNVSVSDLSFPLVGPPEPILCHPLSLSLSYNNNSINGSLSADDFDCHNLI 117
76 SLIIDDEALTGOIPPOVG-DLPLQAL-----WFKRLP----- 108
118 SLDLSEN-LVGSIPKSLPFPNLPNPKFLEISGNNSDTIPSSFGFRKLSLNLAGNLS 176
109 -----NLF--GKIPPEISALKDKLSRLSTSLGVP/LFFPOLT 146
177 GTIPASLGNVTLTKELKLAIVNLFSPSQIPQSLQNLTELOVLAAGCNLYCPISLSRLT 236

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QY 216 -----RADPIR-----LDPSGNRLEGDISFLFGPKKRL 244
      ||:|
Db 241 PNSIMWLSLRAFSVRENKLGMIPTNAFKTLHLLEVIMGTNRPHGKIPASVANASHLT 300
      ||:|
QY 245 MLDPSGN---VLSFNFPSRYOEFPSLTYLDLNNH-----QISGSLSSHLAKLD-LQTF 293
      ||:|
Db 301 VIOIYGNLFSGITSGFGRRL---NLTELYLWRNLFOFREDDMGFISDLTNC SKLQTL 356
      ||:|
QY 294 NWSNNLGGKIP 305
      ||:|
Db 357 NLGNNLGGVLP 368
      ||:|

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Search completed: March 13, 2002, 20:56:46
 Job time: 2557 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2002, 20:16:09 ; Search time 33.71 Seconds

(without alignments)
750.221 Million cell updates/sec

Title: US-09-308-140-7

Perfect score: 1756

Sequence: 1 MNISSEFCPLICIMFLCL.....FDRATYLNHNSCLGAPLPEC 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	884.5	50.4	330	2 JQ2262	Polygalacturonase
2	849	48.3	327	2 T10263	probable polygalac
3	844	48.1	327	2 S47965	polygalacturonase
4	819	46.6	329	2 T17033	leucine rich repea
5	632	35.4	342	2 S23764	polygalacturonase-
6	567	32.3	313	2 S60713	polygalacturonase-
7	411.5	23.4	478	2 H86459	hypothetical prote
8	408.5	23.3	371	2 T49908	hypothetical prote
9	401	22.8	480	2 T00971	probable disease r
10	398.5	22.7	512	2 H86459	hypothetical prote
11	378	21.5	976	2 B84652	probable receptor-
12	370	21.1	486	2 B84660	hypothetical prote
13	370	21.1	907	2 A86460	hypothetical prote
14	361	20.0	1232	2 T05322	hypothetical prote
15	348.5	19.8	932	2 T48489	receptor-like prote
16	346	19.7	992	2 T05335	hypothetical prote
17	338	19.2	1064	2 B84665	probable protein k
18	335	19.1	981	2 T50851	receptor protein k
19	330.5	18.8	719	2 T47727	hypothetical prote
20	330.5	18.8	983	2 G84524	probable disease r
21	329.5	18.8	987	2 T50850	receptor protein k
22	327.5	18.7	1002	2 T46033	receptor protein k
23	327.5	18.6	964	2 T49038	hypothetical prote
24	325.5	18.5	905	2 T00475	probable disease r
25	323.5	18.4	1027	2 B85089	receptor protein k
26	322.5	18.4	1013	2 T10659	probable serine/ch
27	322.5	18.3	1120	2 B84717	hypothetical prote
28	322	18.3	988	2 T45717	receptor-kinase 11
29	322	18.3	1143	2 B84431	probable receptor

30	322	18.3	1192	2 T48499	receptor-like prot
31	321.5	18.3	869	2 A71400	probable disease r
32	321.5	18.3	1133	2 E86308	hypothetical prote
33	319.5	18.2	1016	2 T30553	disease resistance
34	317	18.1	702	2 A86383	hypothetical prote
35	316.5	18.0	1123	2 D96756	receptor-like prote
36	315	17.9	967	2 T48210	hypothetical prote
37	315	17.9	1112	2 T10504	disease resistance
38	314.5	17.9	980	2 H84632	probable receptor-
39	313	17.8	1003	2 T05898	hypothetical prote
40	312.5	17.8	766	2 T01817	hypothetical prote
41	312	17.8	1025	2 T45647	receptor protein k
42	311.5	17.7	999	1 S27756	receptor-like prote
43	309.5	17.6	598	2 C96756	receptor-like prote
44	309.5	17.6	960	2 G84652	probable receptor-
45	309	17.6	719	2 T02154	protein kinase hom

ALIGNMENTS

RESULT 1
JQ2262
Polygalacturonase inhibitor precursor - Pyrus communis
C:Species: Pyrus communis
C:Date: 04-Sep-1998 #sequence-revision 04-Sep-1998 #ext-change 21-Jan-2000
C:Accession: JQ2262
R:Stoltz, H.U.; Powell, A.L.T.; Damon, S.E.; Greve, L.C.; Bennett, A.B.; Labavitch, J.
Plant Physiol. 101, 133-138, 1993
A:Title: Molecular characterization of a polygalacturonase inhibitor from Pyrus commu
A:Reference number: JQ2262
A:Accession: JQ2262
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-330 <STO>
A:Cross-references: GB:109264; NID:q169683; PID:AAA33865.1; PID:q169684
C:Superfamily: polygalacturonase-inhibiting protein; leucine-rich alpha-2-glycoprotei
F:144-167/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 50.4%; Score 884.5; DB 2; Length 330;

Best Local Similarity 55.0%; Pred. No. 1.1e-64;

Matches 182; Conservative 40; Mismatches 106; Indels 3; Gaps 3;

QY	3	1ESSFCPLICIMFLCLPNLSSORCNNDKQALLQITALKNPTITDTSVDDCCGW	62
DB	1	MEKFTSTFLSTLTFSSVNPALSDLCNPDKKVLLQIKKAFEDPYVLASWKSDDCCDW	60
QY	63	DVECESTNRIITSLTIODEALTQIPQVCDLPYLQALMFRKLPNLFGKIPETISALK	122
DB	61	YCVTCSTTNRIINSLITFAGQ-VSGQIPALVGDLPYLELLEFKQPNLNGPIQPAIAKAK	119
QY	123	DKSLRSTLSLSPVLPFPOLTKITCLDLSFNKLLGVIPOLSTLPNKLALHLEENEL	182
DB	120	GKSLRSTLSTNLSGVPDLSQKNLTFDLSPNNLTGAIIPSSLSELPALGRLDRNKL	179
QY	183	TGEIPITFGNFGAS-FDITLSNQLTGFPVKTFARADPIRLDESGRLGDSIFLGPXK	241
DB	180	THPIPSFOFIGNPDVLSHNLGSGNIPISFQMDFTSIDLSRNKLGDSVIFGLXK	239
QY	242	RLMDLFGNLSFNSRVOEPFSLTYLDLNNHNSGSLSELAKLDQTFNVSNNNC	301
DB	240	TTOYDLSNRLNLEFNLSKY-EPTSLTSLDINHKNKTYGSIPEVFTOLNOLFNVSNRNC	298
QY	302	GRIPTGNNLQREDRTAYLHNSCLGAPLPEC	332
DB	299	GQIPVGKRLQSFDEXSYFNNRCLGAPLPSC	329

RESULT 2
T10263
probable polygalacturonase-inhibiting protein - sweet orange
C:Species: Citrus sinensis (sweet orange)

OY 269 -YLDLNHNQISGS-----ISSELAKD----- 269
 Db 371 FYIDLSENEISGSLTWPFENLAHNLFEQASGNKLFEDMGKLNLSERLESIDLNRNLIIFGK 430
 OY 290 -----LQFFNVSNDNLCKKIPFGNGLQRFDRFAYLHNSCICGAPLPEC 332
 Db 431 VPMVAKLQKLNLSHNLGCKLP---VTKFPASAFVGNDCICGSPUSPC 476
 RESULT 8
 T49908
 hypothetical protein T24H18.110 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse ear cross)
 C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: T49908
 R:Bevan, M.; Robben, J.; Gyomai, B.; Volckaert, G.; Bancroft, I.; Mewes, H.W.; Rudd,
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 225024
 A:Accession: T49908
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-371 <BEV>
 A:Cross-references: EMBL:AL353013; GSPDB:GNO0063; ATSP:T24H18.110
 C:Genetics: A:Experimental source: cultivar Columbia; BAC clone T24H18
 A:Gene: ATSP:T24H18.110
 A:Map position: 5
 Query Match 23.3%; Score 408.5; DB 2; Length 371;
 Best Local Similarity 30.2%; Pred. No. 8.8e-26;
 Matches 113; Conservative 55; Mismatches 159; Indels 47; Gaps 8;
 OY 1 MNIESFCPLICMIFCLPNLASQRCNNNDKQALQIKTALKNPTI--TDSWSDDD 58
 Db 1 MDRKSLVILLTNVVFLLSTVHS--CLPSDRAALFERAKLNEFYIGVFTWKGLDC 58
 OY 59 CCGMDLVECOETSNRIISLIIDDE-----ALTGQIPROYGDLPIYQALMFRK 106
 Db 59 CKWYGVSCDPMNRVRVAGITLRGSEDDPLFOKAKRSQGLMGSISPICKLTRLISGLIIAD 118
 OY 107 LPLNFGKIPPEISALKDLKSLRSLSTSLSGVPLFPFQPLKTLCLDLSFKKLGIVIPOL 166
 Db 119 WKGISVITPCIEHLPLRLHLDLVGNKFSGVITANIGKLLRLVNLADNHLGVIPPSI 178
 OY 167 STPLNKAHLERNELTGEIPDIFGNFAGSPDIYLSHNLGTFVPTKTFAR---ADPTRL 222
 Db 179 TRLVSLSHLDLRNNNISGVIPRDIQRLKMYSRVLISGKISQIOPSLRIRYRLAD---L 235
 OY 223 DFGNRLREGDIFLFGKRRKLEMLDFSGNLS-----FNFSRVO 261
 Db 236 ELSMNRLTGPISAFGMSVATLNDGNLISMPISGLASSISNLSNGLITGIPN 295
 OY 262 EPPPS--LTLYLDLNHNQISGSLSEL-AKLDLOTFNVSNDNLCKKIPFGNGLQRFDRFAY 318
 Db 296 TFGFRSYFTVLDLANNRNLQGPISATTAASFIGHLVSHNHLGCKKIPMGSPFDHLATSP 355
 OY 319 LHNSCICGAPLPEC 332
 Db 356 AYNAICLCGKPLGNC 369
 RESULT 9
 T00971
 probable disease resistance protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse ear cross)
 C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
 C:Accession: T00971; G84659
 R:Rounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, April 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.
 A:Reference number: Z14161

A:Accession: T00971
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-480 <ROU>
 A:Cross-references: EMBL:AC002505; NID:g2739359; PID:g2739389
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Molnar, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umeyam, L.; Tallon,
 euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: G84659
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-480 <STO>
 A:Cross-references: GB:AE002093; NID:g2739389; PID:AA014512.1; GSPDB:GNO0139
 C:Genetics: A:Gene: T9J22.5; AT2g26380
 A:Map position: 2
 Query Match 22.8%; Score 401; DB 2; Length 480;
 Best Local Similarity 26.0%; Pred. No. 5e-25;
 Matches 123; Conservative 65; Mismatches 121; Indels 164; Gaps 17;
 OY 15 MFLCLPNLASQRCNNNDKQALQIKTAL-KNPT-ITDSWSDDDCGMDLVECOETSN 72
 Db 15 VIFLRCLNPTAATCHPDEAGLAFKSGITKDPGSLTWMKGTCCSMNGVSC-PNCG 73
 OY 73 RIISLI--TDDDA---LTGQIPROYGDLPIYQALMFRKLPNLFQKIPPEISALDKSL 127
 Db 74 RVVLTIRIESDAGIFLGGTISPSLAKLQHLGEGVFINLKNITGPFPPFLRPLRLKYV 133
 OY 128 RLSTSLSGVPLFPFQPLKTLCLDLSFKKLGIVIPPOS-----TLP 170
 Db 134 YLENTLSGPLPANICALNRLDITLYKGNRFISIPSSISNLRNLVNLGNNLTGTIP 193
 OY 171 ---NLKA---LHLERNELTGEIPDI----- 190
 Db 194 LGIANLKLSINLNLDCNRLSGTIPDIFKSMNLRILTLNRNFSCKLPPSIASLAPVLA 253
 OY 191 ----GNFGSPDIYLSH-----NOLTFVPTKTFAR-----ADP- 219
 Db 254 LELGNNLSGSIPIYSRVALDPLDLSKNRFSGAVPKSLAKTLKIANINLSHNLITNPF 313
 OY 220 -----I 220
 Db 314 PVLNKNYILTLTDLNKNKFMETIPFWTSASILGSLAKGKIMSLDDMKTRQDLYV 373
 OY 221 RUDSGNRLGCD-ISFLFGPKRRKLEMLDFSGVLSNFSRVODEPPPSLTYLDLNHNQISG 279
 Db 374 SIDLSNEISGSPRLFKG-AGQLREFRMSGKRLFDKRL--SFSTTLTDLNRLVYG 431
 OY 280 SUSEELAKLDLOTFNVSNDNLCKKIPFGNGLQRFDRFAYLHNSCICGAPLPEC 332
 Db 432 KVPARYA--GLKTLNLSQNLGCKLP---VTKFPESYAGNDICGSPUSPC 478
 RESULT 10
 G84659
 hypothetical protein AAG26075.1 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse ear cross)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: G84659
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conny, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719

A;Accession: G86459

A;Status: preliminary

A: molecule type: DNA

A;Residues: 1~512 <STO>

A:Cross-references: GB:AE005172; NID:g10998936; PIDN:AAG26075.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match	22.78;	Score 398.5;	DB 2;	Length 512;
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Best Local Similarity 26.5%; Pred. No. 8.7e-25;

Matches 127; Conservative 63; Mismatches 135; Indels 155; Caps 16;

QY	3	IESFFCPLICIMFIFLCPNLPLNSASORCNNDKALLQIKAL-KNP-INDSVSDDCC	60
Db	36	MNSFLLTFEFVEVIFLQOLNPNTGAATCHPDEAGLLAFKAGITRDRPGIILSSMKKGAC	95
QY	61	GWLDVECDENSRILISLTI--QDDEA---LTGQIPVOYGDPYLQALMFR-----	105
Db	96	SMNGTC-LTTIDRVASALVAGQADVASSFISGLTISPLAKLKHLDGIFYFLDLKNITGSP	154
QY	106	-----KLNP-----LFGKIPDEEISALKDLSLSTSLSGAPVLPFPOLTKTJCL	151
Db	155	QFLQLPLMKVYIENNRRSGLTPANIGALSQLEAFSEEGNRRFGPIRPSISNTLLTOL	214
QY	152	DLSFNKLGVIPOLSTLPLKALHLERNELTGEIPDI-----GNFACS--	196
Db	215	KLGNNLLGTITPLGVANLKMSYLNLCGNRLTGPIDIFKSMPELRSLTSLRNGFSGNLP	274
QY	197	PDI-----YLSHNQLTGVPRKFFARADPI-RUDFSGNRLGEOISLTFGPKKRLEM	245
Db	275	PSIASLAPILRFLELGNHKLSGTIPNLSMFKAADTDLISKNRSGVIPKSFANLTKIEN	334
QY	246	LDFSGNV-----LSFNSRVOEFPPLT-----	268
Db	335	LDLSHNLITDPEFPLVANKGIESDLSITNOCHLNTIPKMWISSPIITSKLAKGICKMSLD	394
QY	269	-----YLDLNNHOISGS-----LSSELAKL-----	298
Db	395	DMKPAQTEFFYQFIDLSENETGSPARELNTQTEYLVEFKAGANKRLRFDMGLTTPAKTLTTL	454
QY	289	-----DLQTFNNSDNNLCKGIPPGGMLQFDRATAYLHNSCJLGAPELPEC	332
Db	455	DISRNLVFGKVPANVAGIKTLTNHNLCKPLP-----VTFEPASAFAGNDCOLGSPISLSP	510

Query Match	21.5%	Score 378;	DB 2;	Length 976;
Best Local Similarity	31.48;	Pred. NO. 9.5e-23;		

Matches 113; Conservative 47; Mismatches 120; Indels 80; Gaps 11;

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QY 23 L$A$QPCNNNDK$ALLOI$K$TALK--NPTITDS$W$--DDDCGNDLVECE$TS$RIISLI 78
Db 16 L$LA$VAT$SE$G$ATLLEIKK$S$F$K$DVNNV$YD-WT$T$S$SDVC$V$M$RG$V$CE$IV$T$F$V$N$A$LN 74
QY 79 IODDEAL$TG$OIP$OV$GDLP$Y$O$AL$W$F$K$LP$N$LF$G$K$I$P$E$B$IS$A$K$D$K$S$R$S$T$S$LS$GPV 138
Db 75 L$SD$N-LDGEI$S$P$A$IG$P$K$S$L$S$ID$RG-NR$LS$O$ID$E$ID$O$C$S$L$O$N$L$D$S$F$N$E$LS$GDI 132
QY 139 P$P$E$P$O$L$T$K$T$C$D$L$S$F$N$K$L$G$V$IP$O$L$S$T$P$N$K$A$L$H$E$N$E$L$T$G$E$I$P$D$F$----- 190
Db 133 P$F$S$K$K$A$K$O$L$E$Q$D$L$K$K$N$Q$D$IG$P$P$S$T$S$Q$P$N$K$K$I$D$D$A$N$K$S$G$E$I$P$R$I$V$W$E$V$Y$Q 192
QY 191 -----GN$F$A$G--$P$D$Y$-----LS$H$Q$LT$G$F$V 210
Db 193 L$G$L$G$N$N$L$V$G$N$I$S$P$D$L$O$LT$G$L$M$Y$F$D$V$R$N$N$S$T$G$S$I$P$E$T$IG$N$C$T$A$F$O$V$L$D$S$T$Y$N$Q$T$G$E$I 252
QY 211 P$K$T$R$A$D$P$I$N$L$D$S$G$N$LE$G$D$I$S$F$L$G$P$K$R$E$L$M$L$P$F$S$G$N$V$L$S$F$N$S$R$V$----- 260
Db 253 P$F$D$G$F$O$V$A$T$L$S$Q$G$N$D$S$K$I$P$S$V$IG$L$M$A$L$V$D$L$D$S$G$N$L$S$G$S$I$P$I$L$G$N$T$F$T$E$K$L 312
QY 261 -----Q$E$P$P$-----S$L$Y$D$L$N$H$N$O$S$G$L$S$E$B$A$K-L$Q$T$F$N$S$D$N$N$L$C$K$I$P 305
Db 313 Y$L$H$N$K$L$T$G$S$I$P$E$L$IG$N$M$S$K$L$A$Y$L$E$D$N$H$N$T$G$E$I$P$E$L$G$K$T$L$D$F$L$V$A$N$N$D$L$E$P$I$P 372

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Query Match	21.1%;	Score 370;	DB 2;	Length 486;
Best Local Similarity	26.6%;	Pred. No. 1.7e-22;		
Matches 122;	Conservative 55;	Mismatches 133;	Indels 148;	Gaps 15;

[illegible]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 13, 2002, 20:56:05 ; Search time 23.91 Seconds
(without alignments)
509.106 Million cell updates/sec

Title: US-09-308-140-7

Perfect score: 1756

Sequence: 1 MNIESSRCPILICIMIFCL.....FDRAYLHNSCLGAPLPEC 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	884.5	50.4	330	1	PGIP_PYRCO
2	622	35.4	342	1	PGIP_PHAVU
3	311.5	17.7	999	1	RLK5_ARATH
4	273	15.5	980	1	CLV1_ARATH
5	236	13.4	674	1	TM11_ARATH
6	227	12.9	942	1	TM11_ARATH
7	192	10.9	395	1	FLIT_DROME
8	185.5	10.6	1256	1	FLIT_DROME
9	175.5	10.0	2145	1	CYAA_PODAN
10	172	9.8	582	1	SHO2_MOUSE
11	169	9.6	1839	1	CYAA_SACKL
12	164.5	9.4	2300	1	CYAA_NEUCR
13	163	9.3	782	1	CHAO_TRICA
14	160.5	9.1	476	1	GP4d_LEIAM
15	158	9.0	376	1	FMOD_MOUSE
16	158	9.0	582	1	SHO2_MOUSE
17	157.5	9.0	343	1	LUM_CHICK
18	157.5	9.0	713	1	GAC1_HUMAN
19	154.5	8.8	373	1	FMOD_BOVIN
20	153.5	8.7	603	1	AL5_MOUSE
21	150	8.5	376	1	FMOD_RAT
22	149.5	8.5	605	1	AL5_PAPHA
23	147	8.4	359	1	PGS2_HUMAN
24	146.5	8.3	605	1	AL5_HUMAN
25	146.5	8.3	2493	1	CYAA_HUMAN
26	145	8.3	376	1	FMOD_HUMAN
27	144.5	8.2	338	1	LUM_HUMAN
28	143	8.1	382	1	PARC_HUMAN
29	143	8.1	1315	1	CHAO_DROME
30	142.5	8.1	1315	1	CHAO_DROME
31	142	8.1	331	1	PLIB_AGRBL
32	142	8.1	536	1	CBP8_HUMAN
33	142	8.1	560	1	GPV_HUMAN

34	141	8.0	277	1	RSU1_HUMAN	Q15404 homo sapien
35	138.5	7.9	312	1	AZGL_HUMAN	P02750 homo sapien
36	138.5	7.9	567	1	GPV_MOUSE	O08742 mus musculu
37	138.5	7.9	1257	1	FLIH_MOUSE	P34268 caenorhabdi
38	137	7.8	1257	1	FMOD_CHICK	P51887 gallus galli
39	137	7.8	2026	1	CYAA_YEAST	P08678 saccharomyc
40	136	7.7	360	1	PGS2_PIG	O9XSD9 sus scrofa
41	135.5	7.7	1097	1	TOLL_DROME	P08953 drosophila
42	135	7.7	360	1	PGS2_BOVIN	P21793 bos taurus
43	132	7.5	354	1	PGS2_MOUSE	P28654 mus musculu
44	131.5	7.5	357	1	PGS2_CHICK	P28675 gallus galli
45	131	7.5	277	1	RSU1_MOUSE	O01730 mus musculu

ALIGNMENTS

```

RESULT 1
PGIP_PYRCO STANDARD: PRT: 330 AA.
AC 005091.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE POLYGALACTURONASE INHIBITOR PRECURSOR (POLYGALACTURONASE-INHIBITING
DE PROTEIN).
CN PGIP.
OS Pyrus communis (Pear).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids I; Rosales; Rosaceae; Pyrus.
OX NCBI_TaxID=23211.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BARTLETT;
RX MEDLINE=94151422; PubMed=8108494;
RA Stotz H.U., Powell A.L., Damon S.E., Greve L.C., Bennett A.B.,
RA Labavitch J.M.;
RT "Molecular characterization of a polygalacturonase inhibitor from
RT Pyrus communis L. cv Bartlett.";
RT Plant Physiol. 102:133-138(1993).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=CV. BARTLETT; TISSUE=Fruit;
RX Abu-Goukh A.A., Greve L.C., Labavitch J.M.;
RT "Purification and partial characterization of 'Bartlett' pear
RT polygalacturonase inhibitors.";
RT Physiol. Mol. Plant Pathol. 23:111-122(1983).
CC -!- FUNCTION: INHIBITOR OF FUNGAL POLYGALACTURONASE. IT IS AN
CC IMPORTANT FACTOR FOR PLANT RESISTANCE TO PHYTOPATHOGENIC FUNGI.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
CC -!- SIMILARITY: TO P.VULGARIS POLYGALACTURONASE INHIBITOR.
CC
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL: L09364; AAA33865.1; -
DR PIR: J02262; J02262.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00560; LRR; 4.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00370; LRR; 5.
KW Signal.
FT SIGNAL 1 24
FT CHAIN 25 330
FT CHAIN 330
SEQUENCE 330 AA; 36504 MW; 36BA2BCF420393E3 CRC64;

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Query Match 50.4%; Score 884.5; DB 1; Length 330;
 Best Local Similarity 55.0%; Pred. No. 4,5e-65;
 Matches 182; Conservative 40; Mismatches 106; Indels 3; Gaps 3;

DR 1 ESSFPCILICMIFCLPILNASQRCNNNDKQALQITALKNPITTSWSDDCG 62
 DR 1 MELKFSFSLSTLSSVLPALSDLCNDDKKVLLQIKAFGDPYVLASMSKSDTDCDW 60
 DB 63 DLVCCDETSNRITLIIODEALTGQIPPOVGDPIYLQALMFKRLPMLFGKIPREISALK 122
 DB 61 YCVICDSTNTINSLTFAGQ-VSGQIPALVGLPYLETLEFHQPNVLGPIDPAIKLK 119
 DB 123 DLKSLRLSTSLSGVPLFPOLFKLCLDLSFKLGLVIRPOLSTPNLKALHLENEL 182
 DB 120 GLKSLRLSWNLSSVDFLSQNLTLFLDLSFNLTGALIPSSLEIPNLGALMLDRNKL 179
 DB 183 TGEIPDLFGNFAGS-PDIYLSHNOITGFPVKTFAADPIRLDFSGNLEGDISFLFGPKK 241
 DB 180 TGHIPISFGQIGVNPDLYLSHNLGNSIPFSQMDPTSIDLSRNKLEGDASVIFGLNK 239
 DB 242 RLEMLDPSGNVLSNFRVQEPFPLSYTLDLNHNQISGLSSELAKLDTFNNSDNNLC 301
 DB 240 TTDIVLSRLNLEFNLSEKV-EFPTSLTSLDINHNNKIYGSIPVEFTQLNFOFLVSYNRLC 298
 DB 302 GKIPTEGNLORFRTAYLHNSCLGAPLPEC 332
 DB 299 GQIPVGGKLOSFDEYTFHNRCLGAPLPEC 329

RESULT 2
 ID PCIP_PHAVU STANDARD: PRT: 342 AA.
 AC P35334;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE POLYGALACTURONASE INHIBITOR PRECURSOR (POLYGALACTURONASE-INHIBITING PROTEIN).
 OS Phaseolus vulgaris (kidney bean) (French bean).
 GN Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus; NCBI_TaxID=3885;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC STRAIN=CV, SAXA, AND CV, PINTO; TISSUE=Hypocotyl;
 RX MEDLINE=93272053; PubMed=1303801;
 RA Toubart P., Desiderio A., Salvi G., Cervone F., Darda L., de Lorenzo G., Bergmann C., Darvill A.G., Albersheim P., Cloning and characterization of the gene encoding the endopolylgalacturonase-inhibiting protein (Pgip) of phaseolus vulgaris plant J. 2:367-373(1992).
 RT L.;
 CC - FUNCTION: INHIBITOR OF FUNGAL POLYGALACTURONASE. IT IS AN IMPORTANT FACTOR FOR PLANT RESISTANCE TO PHYTOPATHOGENIC FUNGI.
 CC - SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
 CC - TISSUE SPECIFICITY: FOUND IN SUSPENSION-CULTURED CELLS AND TO A LESSER EXTENT IN HYPOCOTYLS, LEAVES AND FLOWERS.
 CC - SIMILARITY: TO P. COMMUNIS POLYGALACTURONASE INHIBITOR.
 CC - CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
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 CC EMBL: X64769; CAA46010.1; -

DR EMBL: A23205; CAA01664.1; -
 DR PIR: S23764; S23764.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR Pfam: PF00560; LRR: 3
 DR SMART: SM00370; LRR: 5.
 KW Signal; Glycoprotein; Cell wall.
 FT SIGNAL 1 29
 FT CHAIN 30 342
 FT CARBOHYD 64 64
 FT CARBOHYD 141 141
 FT CARBOHYD 303 303
 FT CARBOHYD 181 181
 FT VARIANT 207 207
 FT VARIANT 239 239
 FT VARIANT 253 253
 FT VARIANT 263 263
 FT VARIANT 267 267
 FT VARIANT 300 300
 FT VARIANT 320 320
 FT VARIANT 326 326
 FT VARIANT 340 340
 SQ SEQUENCE 342 AA: 37101 MW: 950F94E0D2A39598 CRC64;

Query Match 35.4%; Score 622; DB 1; Length 342;
 Best Local Similarity 41.0%; Pred. No. 1.2e-43;
 Matches 141; Conservative 56; Mismatches 127; Indels 20; Gaps 7;

QY 2 NIESSFCPLICMIFCLPILNASQRCNNNDKQALQITALKNPITTSWSDDCG 61
 DB 5 NIPVTSSSLIILVILVSLRTALSELCPQDQKQALQIKKIDNPITTSWSDTDCN 64
 QY 62 -WDVCCDETSN--RIISLIODEALTGQ-----IPPOVGDPIYLQALMFKRLP 110
 DB 65 RTWLGVLCDTDTQTYRNNL-----DLSGHNLKPYPISSLANLYLFLYIGGINL 118
 QY 111 FGKIPREISALKDLSRLSTSLSGVPLFPOLTKLCLDLSFNKLGLVIRPOLSTLP 170
 DB 119 VGPPIPAIAKLQDLHYLYIHTNVSGAIPDLQIKTLVTLDSYNALSTLPSPSSLP 178
 QY 171 NLKALHLENELTGEIPDLFGNFAG-SPDIYLSHNOITGFPVKTFAADPIRLDFSGNRL 229
 DB 179 NLGCIFFDQGRISGAIPDSYSGFSKLFMTAMTISRNRITGKIPPTFALNLAFVDSLNNML 238
 QY 230 EGDISFLFGKRLLEMLDPSGNVLSNFRVQEPFPLSYTLDLNHNQISGLSSELAKL 289
 DB 239 EGDASVLFSGDKMTKRIHLAKNSLAFDLGKV-GLSKNLGLDLRNNRIYGTLPGLTQLK 297
 QY 290 -LQTFNNSDNNLCGKIPTEGNLORFRTAYLHNSCLGAPLPEC 332
 DB 298 FLOSLVSNFNLGCEIPQGNLKRFDVSYANNKCLGGSFLPEC 341

RESULT 3
 ID RLKS_ARATH STANDARD: PRT: 999 AA.
 AC R47775;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR (EC 2.7.1.-).
 GN RLKS OR ATG28490 OR F2109.180.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX MEDLINE=94035150; PubMed=8220453;
 RA Walker J.C.;

RT "Receptor-like protein kinase genes of Arabidopsis thaliana."
 RL Plant J. 3:451-456(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA.
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Poll T., Dueterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Anstorge W., Brandt P., Givelli L.A., Kieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Macho R., Mueller M.,
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtke T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Bouty M., Bancroft I.,
 RA Vos P., Hohenseil J., Zimmermann M., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Glymoprez B., Chang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastlaens I., Aert R., Deleor E.,
 RA Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Slaveren M., Dirkse W.,
 RA Moollan P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Bysschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail A., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
 RA Peltett A., Rajandream M.-A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Blocker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Mearse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Faltmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argitell A., Vitale D., Liguori R., Piravandi E.,
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chedorf F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse A.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Biele C.,
 RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedha N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Lattelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mink P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Krimer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Gessel C., Layman D.,
 RA Du H., All J., Berhoff A., Jones K., Dione K., Cotton M., Joshi C.,
 RA Antoniou B., Zizanie M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Grenat S., Shohdy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,
 RA Chen E., Marra M., Martensen R., McCombie W.R.,
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana."
 RL Nature 402:769-777(1999).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=94368830; PubMed=8086440;
 RA Horn M.A., Walker J.C.,
 RT "Biochemical properties of the autophosphorylation of RLK5, a
 receptor-like protein kinase from Arabidopsis thaliana."
 RL Biochim. Biophys. Acta 1208:65-74(1994).
 CC -1- COFACTOR: HAVE SIGNIFICANTLY GREATER ACTIVITY IN THE PRESENCE OF
 MN2+ THAN MG2+.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ROOTS AND ROSETTES.
 CC -1- PTM: AUTOPHOSPHORYLATED ON SERINE AND THRONINE RESIDUES.
 CC -1- SIMILARITY: IN THE C-TERMINAL REGION; BELONGS TO THE SER/THR
 CC FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPEATS (LRR).
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CC or send an email to license@isb-sib.ch.
 CC -----
 DR EMBL: M84660; AAA32859.1;
 DR EMBL: AL021749; CAA16889.1;
 DR EMBL: AL161572; CAB79651.1;
 DR HSSP: P00523; 2PTK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR-out.
 DR InterPro: IPR002290; Ser_Chr_kin_actsite.
 DR Pfam: PF00560; pkinase; 1.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SM00370; LRR; 17.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Transmembrane; Glycoprotein; Phosphorylation; Leucine-rich repeat;
 KW Repeat; Signal.
 FT SIGNAL 1 14
 FT CHAIN 15 999
 FT DOMAIN 15 621
 FT TRANSMEM 622 641
 FT DOMAIN 642 999
 FT REPEAT 88 112
 FT REPEAT 114 138
 FT REPEAT 138 161
 FT REPEAT 163 186
 FT REPEAT 188 211
 FT REPEAT 235 261
 FT REPEAT 263 283
 FT REPEAT 283 306
 FT REPEAT 306 330
 FT REPEAT 332 353
 FT REPEAT 354 378
 FT REPEAT 402 426
 FT REPEAT 426 450
 FT REPEAT 452 474
 FT REPEAT 498 522
 FT REPEAT 524 547
 FT REPEAT 549 567
 FT REPEAT 567 592
 FT DOMAIN 683 968
 FT CARBOHYD 98 968
 FT CARBOHYD 102 102
 FT CARBOHYD 150 150
 FT CARBOHYD 185 185
 FT CARBOHYD 210 210
 FT CARBOHYD 269 269
 FT CARBOHYD 282 282
 FT CARBOHYD 452 452
 FT CARBOHYD 576 576
 FT NP_BIND 689 697
 FT BINDING 711 711
 FT ACT_SITE 819 819
 FT MUTAGEN 711 711
 SO SEQUENCE 999 AA; 109095 MW; F5793D899EA0C6A7 CRC64;
 CC -----
 Query Match 17.7%; Score 311.5; DB 1; Length 999;
 Best Local Similarity 26.6%; Pred. No. 1,1e-17;
 Matches 115; Conservative 49; Mismatches 125; Indels 143; Gaps 16;
 CC -----
 QY 7 FCPILICIMFLCLPNTSASORCNNDKQALLQIKTALKNPTIT-DSWVSDDC--CGMD 63
 DB 3 YCLLLCLCLSTYIPSLT-----NDATILRQAKKLGLSDPAQSLSSSDNDVTPCKWL 57
 QY 64 LVEDEFTSN-----RII 75
 DB 58 GVSCDATSNVSVSLSSFMVLGPPSILCHLPJLSLSLYNNSINGSLADDFDTCHNLT 117
 QY 76 SLIIIDDEALIGQIRPQVG-DLPRYLQAL-----WFRKLP----- 108


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FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 558 558 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 235 235 R -> P (IN REF. 3).
FT CONFLICT 703 703 A -> S (IN REF. 2).
FT CONFLICT 856 856 G -> D (IN REF. 2).
SQ SEQUENCE 980 AA; 107656 MW; B69BD7A7A8863295 CRC64;

Query Match 15.5%; Score 273; DB 1; Length 980;
Best Local Similarity 24.3%; Pred. No. 1,5e-14;
Matches 88; Conservative 47; Mismatches 105; Indels 122; Gaps 8;

QY 85 LTGQIPPOVGDLPYLOALMPFKLPNLFGRKPEETISALKDKLSLSTSLSGVPLFFPQ 144
DB 253 LTGEITPTSINLKHHTL-FLHINNLTGRIPEPLSGVLSKSLDLSINQLTGEIPQSFIN 311
QY 145 LTKLTCGLDLSFNKLCVIPPOLSTLPNLKALHLERNELTGEIPDFGNFAGSPDIYLSHN 204
DB 312 LGMTILINLFNNLYGOIPAEIGELPKLEFEVWENNFTQLPANIANGRNLTAKLDVSDN 371
QY 205 QLTGVPKTFARADPR----- 221
DB 372 HLGLIPKDLCRGEKLEMLLSNNFFGPPIPEELGCKSLTKIRIVKNLNGTVPAGLFPN 431
QY 222 -----LD-----FSG-----NR 228
DB 432 LPLVTIELTDFEFSEBPLVYMSGVDVLDQIYLSNNMFGSIPPAIGFPMQLTFLDRNR 491
QY 229 LQSDISFLFGPKRLMLDFSGN-----VLSFNFSRVQ--EFP----- 264
DB 492 FRONIFREIFELKHLRINSANNITGIPDTSISRCSTLISVLSNNRIINGELPKGINNV 551
QY 265 PSLTYLIDLNHNQISGLSESLAKL-DLQTFNVSNNLCKGIPFGNLQRFDRTPAYLAHNSC 333
DB 552 KNLGTINISGNQLTGIPGIGNMTSLTLDLSFNDLSGRVPLGGQGLVFNENETSGFNTY 611
QY 324 LC 325
DB 612 LC 613

RESULT 5
TML1_ARATH STANDARD: PRT: 674 AA.
AC P33543;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE KINASE-LIKE PROTEIN TMKLI PRECURSOR.
GN TMKLI.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA; TISSUE=Green siliques;
RX MEDLINE=94033320; PubMed=8219075;
RA Valon C., Smalle J., Goodman H.M., Giraudat J.;
RT "Characterization of an Arabidopsis thaliana gene (TMKLI) encoding a
RT putative transmembrane protein with an unusual kinase-like domain.";
RC Plant Mol. Biol. 23:415-421(1993).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO PROTEIN KINASES IN THE C-TERMINUS. BUT DOES NOT

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CC SEEK TO HAVE CONSERVED A KINASE ACTIVITY.
CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
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CC or send an email to license@sib-sib.ch).
-----
CC EMBL: X72863; CAA51385.1; -.
CC PIR: S35397; S35397.
CC PIR: S39476; S39476.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR001611; LRR_out.
CC InterPro: IPR003592; LRR_out.
CC Pfam: PF00560; LRR; 3.
CC Pfam: PF00069; pkinase; 1.
CC SMART: SM00370; LRR; 4.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Leucine-rich repeat;
KW Repeat.
FT SIGNAL 1 25
FT CHAIN 26 674
FT DOMAIN 26 295
FT TRANSMEM 296 323
FT DOMAIN 324 674
FT DOMAIN 373 674
FT REPEAT 98 122
FT REPEAT 122 146
FT REPEAT 147 170
FT REPEAT 172 195
FT REPEAT 198 224
FT REPEAT 226 245
FT REPEAT 245 268
FT CARBOHYD 57 97
FT CARBOHYD 90 90
FT CARBOHYD 95 95
FT CARBOHYD 110 110
FT CARBOHYD 183 183
FT CARBOHYD 195 195
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT SEQUENCE 674 AA; 73353 MW; 533D0A8D8767E253 CRC64;

Query Match 13.4%; Score 236; DB 1; Length 674;
Best Local Similarity 27.1%; Pred. No. 9,6e-12;
Matches 92; Conservative 49; Mismatches 102; Indels 96; Gaps 16;

QY 19 CLPNLSASQRCNNNDKQALL-QIKTALKNPT---ITDSVSDVDDCCGW-----DL 64
DB 23 CGSLSGS-----SDVKLLGKIKKSLQCNSESLLSWNSSVPCQMGVWVWSNGSP 77
QY 65 VRC-DETSRIISLIIODEALTLGOIPVOVGDLPYLOALMPFKLP--NLFGRKPEETISAL 121
DB 78 LQSDISFLFGPKRLMLDFSGN-----HLSTL--QLPSANLTGSLPREIGEF 122
QY 122 KDKLSRLSTSLSGVPLFFPQLTGKTCGLDLSFNKLCVIPPOLSTL-PNLKALHLERN 180
DB 123 SMLQSVFLMINSLSGSIRPLELGTSLSDVDLSGNLALAVLPSPITWNLCDKLVFRHGN 182
QY 181 ELTGEIPDIFGNFAGSPDIYLSHNQLTGFVVPKTFARADPRILDFSGNRLGDISFLFGPK 240
DB 183 NISGVLP-----PAL-----PNSFCG----- 199
QY 241 KRLMLDFSGNVLSTFNFSVQVQEPFPLT-----YLDLNHNQISGLSESLAKLDLOTFN 294
DB 200 -NLQYLDLGNKFS-----GEPFETIRFKGVKSLDLSNNFEGVLPGCLVLESLN 252
QY 295 VSDNNLCKGIPFGNLQRFDRTPAYLAHNS-CLGAPLPPEC 332

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DB 253 LSHNNFSGMLPDFGE-SKFGAEEGNSPSLCGLPKPC 290

RESULT 6

TMK1_ARATH STANDARD: PRT: 942 AA.

AC P43298: (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR (EC 2.7.1.-).

GN TMK1 OR F15E12.4.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Equisetopsida; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustoids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV COLUMBIA.

RX MEDLINE=93076110; PubMed=1332795;

RA Chang C., Schaller G.E., Patterson S.E., Kwok S.F., Meyerowitz E.M., Blecker A.B.;

RT "The TMK1 gene from Arabidopsis codes for a protein with structural and biochemical characteristics of a receptor protein kinase."

RL Plant Cell 4:1263-1271(1992).

RM [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV COLUMBIA.

RA Lin X., Kaul S., Town C.D., Benito M., Greasy T.H., Haas B.J., Wu D., Maiti R., Rongning C.M., Koo H., Fujii C.Y., Uterback T.R., Barnesstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;

RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PROBABLE RECEPTOR.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: FOUND IN MOST TISSUES.

CC -1- PTM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -1- SIMILARITY: CONTAINS 9 LECITINE-RICH REPEATS (LRR).

CC -----

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CC -----

CC EMBL: L00670; AAA32876.1; .

DR EMBL: AC026480; AAC51302.1; .

DR HSSP: P11362.1FCI.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR001611; LRR.

DR InterPro: IPR003592; LRR_out.

DR InterPro: IPR003591; LRR_Typ.

DR InterPro: IPR003290; Ser_thr_kin_actsite.

DR Pfam: PF00560; LRR: 8.

DR Pfam: PF00069; pkinase: 1.

DR SMART: SM00370; LRR: 7.

DR SMART: SM00369; LRR_Typ: 1.

DR SMART: SM00221; STYK: 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP: 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST: 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM: 1.

KW Transmembrane; Serine/threonine-protein kinase; ATP-binding;

KW Transmembrane; Receptor; Glycoprotein; Signal; Repeat;

KW Leucine-rich repeat; Phosphorylation.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 942 PUTATIVE RECEPTOR PROTEIN KINASE TMK1.

FT DOMAIN 24 482 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 483 503 POTENTIAL.

FT DOMAIN 504 942 CYTOPLASMIC (POTENTIAL).

FT REPEAT 87 110 LRR 1.

FT REPEAT 110 133 LRR 2.

FT REPEAT 135 159 LRR 3.

FT REPEAT 185 209 LRR 4.

FT REPEAT 231 253 LRR 5.

FT REPEAT 254 278 LRR 6.

FT REPEAT 280 300 LRR 7.

FT REPEAT 385 408 LRR 8.

FT REPEAT 409 436 LRR 9.

FT DOMAIN 588 869 PROTEIN KINASE.

FT NP_BIND 594 602 ATP (BY SIMILARITY).

FT BINDING 616 616 ATP (BY SIMILARITY).

FT ACT_SITE 717 717 BY SIMILARITY.

FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 942 AA; 102387 MW; 93E30B52FE549DE CRC64;

Query Match 12.9%; Score 227; DB 1; Length 942;

Best Local Similarity 28.8%; Pred. No. 8,1e-11;

Matches 88; Conservative 52; Mismatches 138; Indels 28; Gaps 14;

QY 11 LCICMIFCLPNIASORCNNDKQALQITALKNPITTSWVSDDDCGMDVECDT 70

DB 8 LLEFSTFLL--LLSKADSDGDLSSAMLSKLKSL--NPPSSFGW--SDPDCKWTHIVC--T 61

QY 71 SNRIISLIIDDEALTIQIPQVDPYLAQ--WPKLPNLFKGIPEEISALKDKSL 127

DB 62 GTKRVTRIQIHSLSGLQTLSPDLNLSELELEW--NNISGVPV--SLSGIASLQVL 116

QY 128 RLSTSLSGPPLPEFPQTLTKCLDLSFNKLG--VIRPOLSTLNKAHHERHELGEI 186

DB 117 MLSNNNDSTIPSDVFOGLTSLQSVIEIDNPPKSWEPISLNASALONFSAANVSGSL 176

QY 187 PDIG--NFAASPDIYLSHNOITGFVPTFARADPIRLDFSGNRLGDISFL--FGPKK 241

DB 177 PGCFGPEPEPFLSLHLAFNNLEBELPMSLAGSVOSLMLNGKLTGDIYLAQMTGIAKE 236

QY 242 -RLMDLDSGNVLSFNRSVQEPFPPSLTYLDLNHNQISGLSSLEAKID--LOTNVSDNN 299

DB 237 VMLSHNKFSGLP--DESGIKE---LESLSLRDNSEFTGPVPSLLESIAKVVNLNNH 290

QY 300 LCGKIP 305

DB 291 LQGPVP 296

RESULT 7

D100_ARATH STANDARD: PRT: 395 AA.

AC Q00874;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR (FRAGMENT).

GN DRT100.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Equisetopsida; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustoids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV COLUMBIA;

RX MEDLINE=92390391; PubMed=1518832;

RA Pang O., Hays J.B., Rajagopal I.;

RT "A plant cDNA that partially complements Escherichia coli reca

RT mutations predicts a polypeptide not strongly homologous to RecA
 RT proteins.
 CC Proc. Natl. Acad. Sci. U.S.A. 89:8073-8077(1992).
 CC -i- FUNCTION: THIS PROTEIN IS ABLE TO COMPLEMENT BACTERIAL RECA
 CC MUTATIONS, BUT IT'S NATIVE FUNCTION IN THE PLANT IS NOT KNOWN.
 CC -i- SIMILARITY: CONTAINS 4 LEUCINE-RICH REPEATS (LRR).
 CC -i- SIMILARITY: STRONG TO OTHER EUKARYOTIC RECA-LIKE PROTEIN, SOME, TO
 CC PROKARYOTIC RECA PROTEIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X66482; CAA47109.2;
 CC PIR: A46260; A46260.
 CC PIR: S22863; S22863.
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR003592; LRR_out.
 CC Pfam: PF00560; LRR; 1.
 CC SMART: SM00370; LRR; 3.
 CC TransIt peptide: Chloroplast; leucine-rich repeat; Repeat;
 CC ATP-binding; DNA repair; DNA damage.
 CC NON_TER 1
 CC TRANSIT 74 395 CHLOROPLAST (POTENTIAL).
 CC CHAIN - 74 395 DNA-DAMAGE-REPAIR/TOLERATION PROTEIN
 CC DRT100.
 CC REPEAT 155 180 LRR 1.
 CC REPEAT 250 274 LRR 2.
 CC REPEAT 276 297 LRR 3.
 CC REPEAT 298 322 LRR 4.
 CC NP_BIND 189 196 ATP (POTENTIAL).
 CC SEQUENCE 395 AA: 43810 MW: 48434.33 kDa CRC64:
 Query Match 10.9%; Score 192; DB 1; Length 395;
 Best Local Similarity 22.4%; Pred. No. 1.9e-08;
 Matches 83; Conservative 43; Mismatches 144; Indels 100; Gaps 8;

ID FLII_DROME STANDARD: PRT: 1256 AA.
 AC 024020: Q24088; Q9VRH0;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FLIGHTLESS-I PROTEIN.
 GN FLII OR CG1484.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R; TISSUE=Embryo;
 RX MEDLINE=94068608; PubMed=8248259;
 RA Campbell H.D., Schimanski T., Claudianos C., Ozsarac N.,
 RA Kasprzak A.B., Cotseal J.N., Young I.G., de Couet H.G., Miklos G.L.G.;
 RA "The Drosophila melanogaster flightless-I gene involved in
 RT gastrulation and muscle degeneration encodes gelsolin-like and
 RT leucine-rich repeat domains and is conserved in Caenorhabditis elegans
 RT and humans";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:11386-11390(1993).
 [2]
 RP SEQUENCE FROM N.A., AND VARIANT SER-601.
 RC STRAIN=CANTON-S;
 RX MEDLINE=96129280; PubMed=8582612;
 RA de Couet H.G., Fong K.S.K., Weeds A.G., McLaughlin P.J.,
 RA Miklos G.L.G.;
 RT "Molecular and mutational analysis of a gelsolin-family member encoded
 RT by the flightless I gene of Drosophila melanogaster";
 RL Genetics 141:1049-1059(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RX MEDLINE=98188272; PubMed=9520435;
 RA Maieszka R., de Couet H.G., Miklos G.L.G.;
 RT "Data transferability from model organisms to human beings: insights
 RT from the functional genomics of the flightless region of Drosophila";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3731-3736(1998).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY; TISSUE=Embryo;
 RX MEDLINE=20196012; PubMed=10731138;
 RA Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Fitse E.,
 RA Stapleton M., Harvey D.A.;
 RT "A Drosophila complementary DNA resource";
 RL Science 287:2222-2224(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobary C., Morris J., Moshfegh A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenhach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: MAY PLAY A KEY ROLE IN EMBRYONIC CELLULARIZATION BY
CC INTERACTING WITH BOTH THE CYTOSKELETON AND OTHER CELLULAR
CC COMPONENTS. ALTERNATIVELY, IT MAY PLAY A STRUCTURAL ROLE IN
CC INDIRECT FLIGHT MUSCLE VITAL FOR EMBRYONIC DEVELOPMENT.
CC -1- TISSUE SPECIFICITY: FOUND IN OVARIES, LARVAL FAT BODIES, BRAIN AND
CC ADULT THORAX.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.
CC -1- DOMAIN: CONSISTS OF A LEUCINE-RICH AMINO TERMINAL HALF, WHICH IS
CC LIKELY TO BE INVOLVED IN PROTEIN-PROTEIN INTERACTION, AND A
CC CARBOXYTERMINAL HALF WHICH HAS HIGH SEQUENCE SIMILARITY TO
CC GELSOLIN AND IS THEREFORE LIKELY TO BE INVOLVED IN ACTIN-BINDING.
CC -1- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
CC -1- SIMILARITY: CONTAINS 15 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 4 GELSOLIN-LIKE REPEATS.

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CC or send an email to license@isb-sib.ch).

CC EMBL: U01182; AAC03566.1; -
DR EMBL: AF017777; AAC28407.1; -
DR EMBL: AF132184; AAD34772.1; -
DR EMBL: AE003568; AAF50830.1; ALT_SEQ.
DR HSP: P02640; 2YIL
DR FLYBASE: FBgn0000709; fli1.
DR InterPro: IPR001974; Gelsolin.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00626; Gelsolin; 4.
DR Pfam: PF00560; LRR; 12.
DR PRINTS: PR00019; LEURICHRPT.
DR PRINTS: PR00597; GELSOLIN.
DR SMART: SM00262; GEL; 6.
DR SMART: SM00370; LRR; 3.
DR SMART: SM00369; LRR_typ; 2.
DR Developmental protein; Repeat: Leucine-rich repeat; Polymorphism.
KW Repeat 4
FT REPEAT 29 51 LRR 1.
FT REPEAT 52 74 LRR 2.
FT REPEAT 75 99 LRR 3.
FT REPEAT 100 122 LRR 4.
FT REPEAT 124 145 LRR 5.
FT REPEAT 147 169 LRR 6.
FT REPEAT 171 192 LRR 7.
FT REPEAT 218 241 LRR 8.
FT REPEAT 243 264 LRR 9.
FT REPEAT 265 287 LRR 10.
FT REPEAT 289 312 LRR 11.
FT REPEAT 313 335 LRR 12.
FT REPEAT 336 358 LRR 13.
FT REPEAT 360 381 LRR 14.
FT REPEAT 360 381 LRR 15.

FT REPEAT 499 557 GELSOLIN-Like 1.
FT REPEAT 746 789 GELSOLIN-Like 2.
FT REPEAT 1064 1102 GELSOLIN-Like 3.
FT REPEAT 1165 1206 GELSOLIN-Like 4.
FT VARIANT 601 601 G->S.
FT CONFLICT 1067 1070 STFC->HYFS (IN REF. 5).
FT CONFLICT 1068 1068 T->A (IN REF. 2).
SO SEQUENCE 1256 AA; 143681 MW; CF0056EFAA8DB92 CRC64;

Query Match 10.6%; Score 185.5; DB 1; Length 1256;
Best Local Similarity 30.9%; Pred. No. 2.9e-07;
Matches 81; Conservative 36; Mismatches 120; Indels 25; Gaps 11;

QY 82 DEALTGIPQVGDPLQ--ALMFKRLPLFGKIPKELISALDKSLRSLSGPPV 139
DB 37 DRQLAIPPELHLQLEHLSLNHNLEKIFGEI-TEISCLSL-DLRINQKNGIIP 94
QY 140 LFFPOLTKLCLDLSEFKLGLVIRPOLSTPLNKLALHLENELTGEIPDFGASPD 199
DB 95 ELF-HLEELTLDLSHNKKEV-PEGLERAKNLIVLSNNOIESIPTPLFIHTDLFL 152
QY 200 YLSHNDLTGFVPKTFARADPIRLDFSGNRLGDISFLFGK-----KLEMDFGSNVLS 254
DB 153 DLSHNRLTLPQTRRLINKTLDSHNPLE-----LFQLRQLPSIQSLEVLKMSGTQT 207
QY 255 -PFPKROEPPSLTYLDLHNOISGSLSELAKLDLOTNVDNNGKPIFGNL-QR 312
DB 208 LNLNPPSIDSLANLCEDLSHNSLPKLPDCVNVVYTLVLRISDNELT-ELTAGVELMOR 266
QY 313 FCDRTAYLHN-----SCLGAP 328
DB 267 LESLNLSRNQVALLPALCKLP 288

RESULT 9
CYAA_PODAN STANDARD: PRT: 2145 AA.
AC 001513;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
DE CYCLASE).
OS Podospora anserina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Lasiosphaeriaceae; Podospora.
OX NCBI_TaxID=5145;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96200867; Pubmed=8621071;
RA Loubradou G., Begueret J., Turcq B.;
RT "An additional copy of the adenylate cyclase-encoding gene relieves
RT developmental defects produced by a mutation in a vegetative
RT incompatibility-controlling gene in *Podospora anserina*."
RL Gene 170:119-123(1996).
CC -1- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
CC METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
CC CAMP.
CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.
CC -1- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
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CC or send an email to license@isb-sib.ch).

DR EMBL: LA3413; AAB05642.1; -

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DR InterPro: IPR001054; Guanylt_cyclase.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_tyr.
DR InterPro: IPR003589; LRR_catalytic.
DR InterPro: IPR001932; PP2C_domain.
DR InterPro: IPR000159; RA.
DR Pfam: PR00211; guanylate_cyc. 2.
DR Pfam: PR00360; LRR_13.
DR Pfam: PR00481; PP2C; 1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00044; CYCC; 1.
DR SMART: SM00370; LRR; 5.
DR SMART: SM00369; LRR_TYP; 1.
DR SMART: SM00332; PP2CC; 1.
DR SMART: SM00314; RA; 1.
DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.
KW Lyase; Repeat; Leucine-rich repeat; cAMP synthesis; Magnesium.
FT REPEAT 751 776 LRR 1.
FT REPEAT 778 800 LRR 2.
FT REPEAT 801 824 LRR 3.
FT REPEAT 826 847 LRR 4.
FT REPEAT 848 870 LRR 5.
FT REPEAT 872 894 LRR 6.
FT REPEAT 895 917 LRR 7.
FT REPEAT 919 940 LRR 8.
FT REPEAT 941 965 LRR 9.
FT REPEAT 963 1005 LRR 10.
FT REPEAT 1006 1027 LRR 11.
FT REPEAT 1028 1051 LRR 12.
FT REPEAT 1053 1074 LRR 13.
FT REPEAT 1075 1097 LRR 14.
FT REPEAT 1099 1120 LRR 15.
FT REPEAT 1123 1256 LRR 16.
FT REPEAT 1257 1280 LRR 17.
FT REPEAT 1282 1304 LRR 18.
FT REPEAT 1305 1328 LRR 19.
FT REPEAT 1357 1380 LRR 20.
FT REPEAT 1394 1419 LRR 21.
FT DOMAIN 1445 1710 PP2C-LIKE.
FT DOMAIN 1711 2145 CATALYTIC.
FT DOMAIN 36 41 POLY-SER.
SQ SEQUENCE 2145 AA; 237515 MW; 88E7FE64AC0687D CRC64;
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RESULT 10
SHO2_MOUSE
ID SHO2_MOUSE STANDARD; PRT; 582 AA.
AC 088520;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LEUCINE-RICH REPEAT PROTEIN SHOC-2 (RAS-BINDING PROTEIN SUR-8).
GN SHOC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9837190; PubMed=9674433;
RA Sieburth D.S., Sun Q., Han M.;
RT "SUR-8, a conserved Ras-binding protein with leucine-rich repeats,
RT positively regulates Ras-mediated signaling in C. elegans.";
RL Cell 94:119-130(1998).
CC -I SUBUNIT: SPECIFICALLY BINDS K-RAS AND N-RAS BUT NOT H-RAS IN
CC VITRO.
CC -I SIMILARITY: CONTAINS 20 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF068921; AAC0175.1; -
DR MGD: MGI:1927197; Shoc2.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_tyr.
DR Pfam: PF00560; LRR; 16.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00370; LRR; 8.
DR SMART: SM00369; LRR_TYP; 5.
KW Repeat; Leucine-rich repeat.
FT REPEAT 99 122 LRR 1.
FT REPEAT 122 145 LRR 2.
FT REPEAT 145 168 LRR 3.
FT REPEAT 168 191 LRR 4.
FT REPEAT 193 214 LRR 5.
FT REPEAT 214 237 LRR 6.
FT REPEAT 239 260 LRR 7.
FT REPEAT 262 283 LRR 8.
FT REPEAT 283 306 LRR 9.
FT REPEAT 306 329 LRR 10.
FT REPEAT 331 353 LRR 11.
FT REPEAT 354 377 LRR 12.
FT REPEAT 379 400 LRR 13.
FT REPEAT 401 424 LRR 14.
FT REPEAT 424 447 LRR 15.
FT REPEAT 447 471 LRR 16.
FT REPEAT 473 493 LRR 17.
FT REPEAT 493 516 LRR 18.
FT REPEAT 518 540 LRR 19.
FT REPEAT 540 563 LRR 20.
SQ SEQUENCE 582 AA; 64947 MW; 62C5C082B3CF5F12 CRC64;
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Query Match 9.8%; Score 172; DB 1; Length 582;
Best Local Similarity 26.6%; Pred. No. 1,3e-06;
Matches 76; Conservative 35; Mismatches 113; Indels 62; Gaps 12;
OY 63 DLVECEETSNRIISLIIDDEALTGOIPPOVGDLPYLAIFRKLPNLFKIPPEISALK 122
DB 93 ELNCKRENSMRDLKRSIHIL-PPSVKELTQUTETLYL-VSNKQSLPAEVGCLV 146
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OY 123 DUKSLRSTSLGSPVLPFPOLTKLTCLDLSFNKL-----LG 160
 DB 147 NLMTLASENSLTS-LPDSLDNLKLRMLDLRHKKLRIPSVVRLDSTLTLYLRFNRT 205
 OY 161 VIPPOLSTLPNLKALHLEENELTGEIPDFGNFAGSPDIYLSHNOITGFPVKTFARADPI 220
 DB 206 TVERDIKRLPKLSMLSTIRENIK-QLPAEIGELCNLTITLDAVHNOLE-HLPKEIGNCTOI 263
 OY 221 -RLDFSGNRLEGDISFLFGPKKRLMDFGSNVLSFN-----FSRVQEPFSLT----- 268
 DB 264 TNLDLQHNHL-----LDLPDTIGNLSSLNMLGRNRLSAIPRSLAKCSALE 310
 OY 269 YLDDNHNOIS---GSLSESLAKLDQTFNVSNDNLGKIPFGNIO 311
 DB 311 ELNLNNNISTLPESLSLVLKNSLTL---ARNCPOLYVGGSQ 353
 RESULT 11
 CYAA_SACKL STANDARD: PRT: 1839 AA.
 AC P23466;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).
 GN CYR1.
 OS Saccharomyces kluyveri (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91323718; PubMed=1864503;
 RA Young D., O'Neill K., Broek D., Wigler M.;
 RL "The adenylate cyclase-encoding gene from Saccharomyces kluyveri.";
 CC Gene 102:129-133(1991).
 CC FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
 CC METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
 CC CAMP.
 CC CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
 CC SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.
 CC SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
 CC SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
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 CC or send an email to license@isb.sib.ch).
 CC EMBL: X56042; CAA39513.1; .
 DB PIR: S14564; OYBYK
 DR PIR: J01145; J01145.
 DR InterPro: IPR001054; Guanylyl_cyclase.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR003589; PP2C_catalytic.
 DR InterPro: IPR001932; PP2C_domain.
 DR InterPro: IPR000159; RA.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR Pfam: PF00560; LRR_14.
 DR Pfam: PF00481; PP2C_1.
 DR PRINTS: PR00019; LEURICHREP.
 DR SMART: SM00044; CYCC; 1.
 DR SMART: SM00370; LRR; 4.
 DR SMART: SM00369; LRR_Typ; 3.
 DR SMART: SM00332; PP2C; 1.
 DR SMART: SM00314; RA; 1.

DR PROSITE: PS50125; GUANYLATE_CYCLASES-2; 1.
 KM Lase: Repeat: Leucine-rich repeat: CAMP synthesis; Magnesium.
 FT REPEAT 632 655 LRR 1.
 FT REPEAT 659 679 LRR 2.
 FT REPEAT 680 702 LRR 3.
 FT REPEAT 703 724 LRR 4.
 FT REPEAT 726 748 LRR 5.
 FT REPEAT 749 771 LRR 6.
 FT REPEAT 773 793 LRR 7.
 FT REPEAT 794 818 LRR 8.
 FT REPEAT 820 833 LRR 9.
 FT REPEAT 834 857 LRR 10.
 FT REPEAT 859 879 LRR 11.
 FT REPEAT 880 903 LRR 12.
 FT REPEAT 905 926 LRR 13.
 FT REPEAT 927 949 LRR 14.
 FT REPEAT 951 974 LRR 15.
 FT REPEAT 1004 1025 LRR 16.
 FT REPEAT 1025 1048 LRR 17.
 FT REPEAT 1050 1072 LRR 18.
 FT REPEAT 1074 1096 LRR 19.
 FT REPEAT 1101 1124 LRR 20.
 FT REPEAT 1135 1160 LRR 21.
 FT DOMAIN 1185 1440 PP2C-LIKE.
 FT DOMAIN 1441 1839 CATALYTIC.
 SQ SEQUENCE 1839 AA; 206895 MW; 86A69BCB1F2733CB CRC64;

Query Match 9.6%; Score 169; DB 1; Length 1839;
 Best Local Similarity 23.6%; Pred. No. 1,le-05;
 Matches 86; Conservative 48; Mismatches 122; Indels 108; Gaps 15;

OY 44 LKNPTITDSWYS--DDCCGMDVYECDETSNRITSLT----- 78
 DB 816 LQNLFTLDNRISTFDLDLTRLTLELQ--NPITSMVCGVYMANMTSLSNKAKLSFS. 873
 OY 79 -----IODEALTGQIPPOVDLPYLOALWFRKLPNFGKIPPEISALKDLS 126
 DB 874 AELLSKLPLEKLELNENNLTQLPPEINKLRL--YLSVARNNLESIPDEISDLRSLS 931
 OY 127 LRLSS-----TSLSGVPVLPF-----POLTK-LTCLDLSFN 156
 DB 932 LDIHSNNLRMLMNNLEDELTLNVSNNLTGFGSPAKFPASPPLAKSLDLFSYADN 991
 OY 157 KLGVIIPOLSTENKALHLEENELTGEIPDFGNFAGSPDIYLSHNOITGFPVKTFAR 216
 DB 992 NLDSIMPLVNTFQNLKTLNLYNNFV-EISDL--KQNTLETLYSGNFTSLPGEVQH 1048
 OY 217 ADPIR-LDFSGNR---LEGDISFLFGPKKRLMDFGSNVLSFNFSRVQ-----EPFSL 267
 DB 1049 LRSKLVLMLNKNKLSLPAELSQL-----SRLSVLDVGSNQLKINISYHYDMNRNKKDL 1104
 OY 268 TYLDLNHN---QISGLSSE-----LAKLDQTFNVSNDNLGKIPT 306
 DB 1105 KYLNFSGNKRFEIKSALDPCKNDLSDGLIKQLRVGLMDVTLTKSVKDESVSIRLRT 1164
 OY 307 GGNL 310
 DB 1165 TASM 1168
 RESULT 12
 CYAA_NEUCR STANDARD: PRT: 2300 AA.
 AC Q01631;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).
 GN CR-1 OR NAC.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariales: Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92000795; PubMed=1680356;
 RA Kore-Eda S., Murayama T., Uno I.;
 RT "Isolation and characterization of the adenylate cyclase structural
 gene of Neurospora crassa."
 RL Jpn. J. Genet. 66:317-334(1991).
 CC -1- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
 CC METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
 CC CAMP.
 CC -1- CATALYTIC ACTIVITY: ATP -> 3',5'-CYCLIC AMP + PYROPHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO ADENYLATE CYCLASE CLASS-3 FAMILY.
 CC -1- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
 CC -----
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 CC -----
 CC EMBL: D00909; BAA00755.1; -
 DR InterPro: IPR001054; Guanylt-cyclase.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_tyr.
 DR InterPro: IPR003589; PP2C_catalytic.
 DR InterPro: IPR001932; PP2C_domain.
 DR InterPro: IPR000159; RA.
 DR Pfam: PF00211; guanylate_cyc; 2.
 DR Pfam: PF00560; LRR; 13.
 DR Pfam: PF00481; PP2C; 1.
 DR PRINTS: PRO0019; LEURICHRPT.
 DR SMART: SM00044; CYCC; 1.
 DR SMART: SM00370; LRR; 4.
 DR SMART: SM00369; LRR_TYR; 2.
 DR SMART: SM00332; PP2C; 1.
 DR SMART: SM00314; RA; 1.
 DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.
 KM LRRase: Repeat: Leucine-rich repeat; CAMP synthesis; Magnesium.
 FT REPEAT 867 890 LRR 1.
 FT REPEAT 892 914 LRR 2.
 FT REPEAT 915 938 LRR 3.
 FT REPEAT 938 961 LRR 4.
 FT REPEAT 962 986 LRR 5.
 FT REPEAT 988 1008 LRR 6.
 FT REPEAT 1009 1031 LRR 7.
 FT REPEAT 1033 1055 LRR 8.
 FT REPEAT 1056 1079 LRR 9.
 FT REPEAT 1081 1097 LRR 10.
 FT REPEAT 1098 1120 LRR 11.
 FT REPEAT 1122 1142 LRR 12.
 FT REPEAT 1143 1165 LRR 13.
 FT REPEAT 1166 1188 LRR 14.
 FT REPEAT 1189 1211 LRR 15.
 FT REPEAT 1213 1234 LRR 16.
 FT REPEAT 1349 1369 LRR 17.
 FT REPEAT 1373 1396 LRR 18.
 FT REPEAT 1398 1420 LRR 19.
 FT REPEAT 1422 1445 LRR 20.
 FT REPEAT 1447 1469 LRR 21.
 FT REPEAT 1474 1497 LRR 22.
 FT REPEAT 1513 1538 LRR 23.
 FT REPEAT 1564 1829 PP2C-LIKE.
 FT DOMAIN 1830 2300 CATALYTIC.
 FT DOMAIN 49 52 POLY-SER.
 FT DOMAIN 204 221 POLY-GLN.
 FT SEQUENCE 2300 AA: 254752 MW: 52E79B90E6B17A7B CRC64:

Query Match 9.4%; Score 164.5; DB 1: Length 2300;
 Best Local Similarity 23.8%; Pred No. 3.3e-05;
 Matches 72: Conservative 45; Mismatches 125; Indels 61; Gaps 11;
 QY 30 NNNDKOAL-LQIKTKLNKPTITDSWVSDCCGWDVECDSTNRITSLIODEALTSQ 88
 DB 924 NNNEQALPKSFATASK-----LTYDVSNRRQDDHSELKSLITL 965
 QY 89 IPPQYGDLPYLOALMFRKLPNLFKIPPEISALKDLSRLSSTSLSCGVPPLFPQTLK 148
 DB 966 LKVNLAN-----NCLRSPLPTLGAYKSLRLTINISNFDV-FPSPICELETI 1011
 QY 149 TGLDLSFNKLCVIPPOLSTLPNLKALHLERNELGEPIDGNGFAGSPDIYLSHNLTG 208
 DB 1012 VOLDLSFNS-INNLGDNLMKLPNLEKFTYNNRSLGPSSESVRLDLSRELDIRYQIST 1070
 QY 209 F-VPTFARADPRIRLDFSGNRLEGDISFLCPKRLMLDFSGN-VLSFNSRVOEFPSP 266
 DB 1071 IDVLSDLPLRLTISAD-----HNQISKFSGSFERLRSLKNSPIYKFEYKAPVIP- 1122
 QY 267 LTYDLNNNOISGSLSEELAKDLDTFN-----VSDNNLCGKIPTG-GNLQRFDRYAY 318
 DB 1123 -----QILNLSNQAOLASIDESIDNLMLERLILDSNFFVSLPNOIGNLKKDLHLSM 1173
 QY 319 LHN 321
 DB 1174 ANN 1176
 RESULT 13
 ID CHAO-TRICA STANDARD; PRT: 782 AA.
 AC P82963;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CHAOPTIN (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN) (FRAGMENT).
 GN CHP.
 OS Tribolium castaneum (Red flour beetle).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiformia; Tenebrionidae; Tribolium.
 OX NCBI_TaxID=7070;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GA-1;
 RA Nie W., Stronach B., Panganiban G., Brown S., Denell R.;
 RT "Molecular characterization of telabial and the 3' end of the
 RT tribolium homeotic complex".
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL MORPHOGENESIS. MEDIATES
 CC HOMOPHILIC CELLULAR ADHESION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR SURFACE OF R-CELL PLASMA
 CC MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAOPTIN FAMILY.
 CC -1- SIMILARITY: CONTAINS AT LEAST 21 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF322227; AAK01654.1; -
 DR InterPro: IPR001611; LRR.
 DR Pfam: PF00560; LRR; 29.
 DR PRINTS: PRO0019; LEURICHRPT.
 KW Glycoprotein; Membrane; Repeat; Leucine-rich repeat; Vision.
 FT NON_TER 1 1
 FT REPEAT 43 66 LRR 1.

```

FT REPEAT 67 90 LRR 2.
FT REPEAT 93 116 LRR 3.
FT REPEAT 117 140 LRR 4.
FT REPEAT 141 164 LRR 5.
FT REPEAT 165 188 LRR 6.
FT REPEAT 224 247 LRR 7.
FT REPEAT 249 272 LRR 8.
FT REPEAT 273 296 LRR 9.
FT REPEAT 297 320 LRR 10.
FT REPEAT 321 343 LRR 11.
FT REPEAT 344 367 LRR 12.
FT REPEAT 391 391 LRR 13.
FT REPEAT 395 418 LRR 14.
FT REPEAT 419 444 LRR 15.
FT REPEAT 446 469 LRR 16.
FT REPEAT 491 513 LRR 17.
FT REPEAT 514 537 LRR 18.
FT REPEAT 539 562 LRR 19.
FT REPEAT 615 638 LRR 20.
FT REPEAT 640 663 LRR 21.
FT CARBOHYD 196 196 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 488 488 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 782 AA: 88561 MW: 31146082D4527917 CRC64:

```

Query Match 9.3%; Score 163; DB 1; Length 782;
 Best Local Similarity 26.7%; Pred. No. 1.1e-05;
 Matches 86; Conservative 37; Mismatches 115; Indels 84; Gaps 14;

```

Db 138 NLKSQRKLNKGNKATIAETFOINPELED-----LDLAYN 174
Oy 81 DDEALTGQIPPOVDLPYLOA-LMFRKLPNLF--GKIPREISALDKLSRLSTSLGCP 137
Db 175 SISLSDNITDQVSGLMFVNMSHNKLNLVVAAPVPE-----ODTGLG- 221
Oy 138 VPLFFPOLTKLCLDLSFNKLLGY-----PRLSTLPNKLALHLENNELTGETIPDIFGN 192
Db 222 -----LQNIKYLDLSFNNTSYAKOFFRPVELS-----LMOLYLGHNKLNLNA TKDFGN 270
Oy 193 FAGSPDIYLSHNOITGVPRKTFARADPIR-LDPSGNRLGEGDISFLGPKRKRLMDLDFSGN 251
Db 271 MPRHQVLDLSHNSLYELDFTFRNTKQLQWLDTSHNRISLIPNDLRFELGNLRIVDFSHN 330
Oy 252 VLSEFNRVQVEFPSS-----LTYLDLNHNQI-----SGLSLS--ELAKLDLOTENVSD 297
Db 331 -----RLNSLPONLRFRETGLERLDVSHNLGKLPRLSTLSLASAQTLSLSDLSMNSIS- 382
Oy 298 NNLCGKIPTGSGNLOREPRTAYL 319
Db 383 -----SLSHGQGLARFKCLSLW 399

```

RESULT 14
 GP46_LEIAM STANDARD: PRT: 476 AA.
 ID GP46_LEIAM
 AC P21978;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SURFACE MEMBRANE GLYCOPROTEIN GP46/M-2 PRECURSOR.
 OS Leishmania amazonensis.
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5659;
 RN [1]

```

RP SEQUENCE FROM N.A., AND SEQUENCE OF 33-61.
RC STRAIN-LTB0016;
RX MEDLINE-91046003; PubMed-2236047;
RA Lohman K.L., Langer P.J., McMahon-Pratt D.;
RT "Molecular cloning and characterization of the immunologically
RT protective surface glycoprotein GP46/M-2 of Leishmania amazonensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8393-8397(1990).
CC -I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use by non-profit institutions as long as its content is in no way
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CC
DR EMBL: M38368; AAA29234.1; -.
DR PIR: A36478; A36478.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003592; LRR-Out.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00370; LRR; 3.
KW Antigen; Membrane; GPI-anchor; Signal; Glycoprotein; Repeat.
FT CHAIN 1 32 SURFACE MEMBRANE GLYCOPROTEIN GP46/M-2.
FT PROPEP 421 476 REMOVED IN MATURE FORM.
FT LIPID 420 420 GPI-ANCHOR (POTENTIAL).
FT DOMAIN 107 202 4 X 24 AA TANDEM REPEATS.
FT REPEAT 107 130 1.
FT REPEAT 131 154 2.
FT REPEAT 155 178 3.
FT REPEAT 179 202 4.
FT CARBOHYD 224 224 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 40 40 G -> E (IN REF. 1; AA SEQUENCE).
FT CONFLICT 44 44 K -> T (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 476 AA: 50136 MW: 722F5DDC48C308BB CRC64:

```

Query Match 9.1%; Score 160.5; DB 1; Length 476;
 Best Local Similarity 23.7%; Pred. No. 8.8e-06;
 Matches 54; Conservative 37; Mismatches 92; Indels 45; Gaps 8;

```

Oy 9 PLICTCMIFCLPNLSASQRCNNKQALLQIT-----AKNFTIDSWSDCCG 61
Db 13 PLAAVALLLCSTSSAPVARAGTSDFTGAQKNLTLYLOAFARALPDLDTW-TGSDFCs 71
Oy 62 WDLVECDSTSNRIISLIDDEALTGQIPPOVDLPYLOALMFRKLPNLFKIPREISAL 121
Db 72 WEHITCYSSG-----VQ-----VMMHNV-DYTGTLREMPASV 102
Oy 122 --KDKLSRLS--STLSGVPVLPFPPOLTKLCLDLSFNKLLGYIIPOLSTLPNKLAL 175
Db 103 DYKDVWIALDLDFGACQGLSGTLPSPSSWMKHLIVLDLSTKTSVGLPPEWSMETSAAEL 162
Oy 176 HLENNELTGETIPDIFGNFAGSPDIYLSHNOITGVPRKTFARADPIRLD 223
Db 163 QLENGCLSGSLPTSSMPKRLIVLSGNHFCGCVDPDSKREDD--RLD 208

```

RESULT 15
 FMOD_MOUSE STANDARD: PRT: 376 AA.
 ID FMOD_MOUSE
 AC P50608;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FIBROMODULIN PRECURSOR (FM).
 GN FMOD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

```

RN  (1)
RP  SEQUENCE FROM N.A.
RC  STRAIN-C57BL; TISSUE-Cartilage;
RA  Saemann A.M.K.;
RL  Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: THIS PROTEIN BINDS TO TYPE I AND TYPE II COLLAGEN AND
CC  AFFECTS THE RATE OF FIBRIL FORMATION (BY SIMILARITY).
CC  -1- PTM: BINDS KERATAN SULFATE CHAINS (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
CC  FAMILY.
CC  -1- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL: X94998; CAA64454.1; -.
DR  MGD; MGI:1328364; Emod.
DR  InterPro: IPR001611; LRR.
DR  InterPro: IPR000372; LRR_Nterm.
DR  InterPro: IPR003592; LRR_out.
DR  InterPro: IPR003591; LRR_typ.
DR  Pfam: PF00560; LRR; 9.
DR  Pfam: PF01462; LRRNT; 1.
DR  SMART: SM00370; LRR; 1.
DR  SMART: SM00013; LRRNT; 1.
DR  SMART: SM00369; LRR_TYP; 1.
KW  Glycoprotein; Connective tissue; Extracellular matrix; Proteoglycan;
KW  Repeat; Leucine-rich repeat; Signal.
FT  SIGNAL 1 18
FT  CHAIN 19 376
FT  REPEAT 115 138
FT  REPEAT 139 164
FT  REPEAT 165 185
FT  REPEAT 186 209
FT  REPEAT 210 232
FT  REPEAT 233 253
FT  REPEAT 254 277
FT  REPEAT 278 302
FT  REPEAT 303 322
FT  REPEAT 323 345
FT  CARBOHYD 127 127
FT  CARBOHYD 166 166
FT  CARBOHYD 201 201
FT  CARBOHYD 291 291
FT  CARBOHYD 341 341
FT  DISULFD 334 367
FT  SEQUENCE 376 AA; 43054 MW; 45A9EDDB0BADA85B CRC64;

Query Match 9.0%; Score 158; DB 1; Length 376;
Best Local Similarity 26.0%; Pred. No. 1e-05;
Matches 87; Conservative 49; Mismatches 115; Indels 84; Gaps 20;

OY 8 CPILCIIMFLCLPNLSASQRCNNNDKQALLQIKTALKNPITTSWSD-----DDCCG 61
DB 76 CPOEDCDP-----PNEPTAMVCDNRNLKYLPEFVPSRMKYVFQNNQISAIQGVFDNATG 130
OY 62 --W-----DLVCDQTSNRITIS-----LIQDDALT---GQIPROYGDLPIYLQALWFR 105
DB 131 LLMVALHGNOITSDVGVGRKVSFKLRLHLRLYLIDHNNLITRMPGLRSLREL-HLDHNOIS 189
OY 106 KLPLNFGKIPRISALKDLSRLS-----STLSGVPVLPFPQLTAKLCLDLSFNKL 158
DB 190 RVPN-----NALRGLRNLTLALYLNHNNEIQGVSSMRG-----LRSLLLDLSYNNHL 235
```

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OY 159 LGVIPPQLSTLPNKLALHLERNELTGELPIDIFGNFAGSPD---IYLSHNOLT--GFVPKT 213
DB 236 RRV-PDGLPSA--LEQLYLEHNNVY-TVPDST--FRGSPKLLLYRLSHNSLNNGLATNT 289
OY 214 FARADPIRLDFSGNRLQEDISFLFGPKKRLEMLDFSGN-----VLSP-----NFSRV 260
DB 290 FNSSSLLELDLSYNOLOK----IPVNTNLENLYQGGRINRNEFSSISFCYVDVNVNFSKL 345
OY 261 QEPFPSLYLDLNNQISGSLSSSELAKLDTQTFNV 295
DB 346 Q-----VLRIDGNEIKRSAMPVDPAPLCLRLANL 373
```

Search completed: March 13, 2002, 21:02:07
Job time: 362 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 13, 2002, 20:56:50 ; Search time 56.08 Seconds
(without alignments)
865.949 Million cell updates/sec

Title: US-09-308-140-7
Perfect score: 1756
Sequence: 1 MNIESSCPLICIMIFCL.....FDRATVHNSCLGAPLPEC 332

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

- Database : SPTREMBL.17:*
- 1: sp.archaea:*
 - 2: sp.bacteria:*
 - 3: sp.fungi:*
 - 4: sp.human:*
 - 5: sp.invertebrate:*
 - 6: sp.mammal:*
 - 7: sp.mhc:*
 - 8: sp.phage:*
 - 9: sp.plant:*
 - 10: sp.recent:*
 - 11: sp.virus:*
 - 12: sp.vertibrate:*
 - 13: sp.vertebrate:*
 - 14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	100.0	332	10	092438 daucus caro
2	937.5	53.4	327	10	038695 actinidia c
3	894	50.9	333	10	09AXP4 Q9AXP4 vilis vinif
4	877.5	50.0	330	10	P93270 malus domes
5	866.5	49.3	330	10	09LKO8 Q9LKO8 prunus maha
6	851	48.5	327	10	022532 prunus arme
7	851	48.5	327	10	080399 citrus sp.
8	851	48.5	327	10	09SAR2 Q9SAR2 citrus sp.
9	850	48.4	327	10	080420 citrus unsh
10	849	48.3	327	10	096401 citrus sine
11	844	48.1	327	10	040160 lycopersico
12	843	48.0	327	10	064465 citrus jamb
13	842.5	48.0	327	10	09SAY9 Q9SAY9 citrus iyo
14	839.5	47.8	327	10	09ZMH6 Q9ZMH6 poncirus tr
15	838	47.7	327	10	09ZMH5 Q9ZMH5 fortunella
16	830.5	47.3	327	10	080421 citrus iyo
17	819	46.6	329	10	038738 antirrhinum
18	813	46.3	327	10	064460 citrus jamb
19	808	46.0	303	10	09SED5 Q9SED5 eucalyptus

ALIGNMENTS

20	808	46.0	303	10	Q9SED2	Q9SED2	eucalyptus
21	807	46.0	303	10	Q9SED1	Q9SED1	eucalyptus
22	802	45.7	303	10	Q9SED3	Q9SED3	eucalyptus
23	794	45.2	303	10	Q9SED4	Q9SED4	eucalyptus
24	792.5	45.1	330	10	Q9M5J9	Q9M5J9	arabidopsis
25	784	44.6	326	10	Q9M5J8	Q9M5J8	arabidopsis
26	784	44.6	330	10	Q9M5J8	Q9M5J8	arabidopsis
27	719	40.9	325	10	Q9M7E7	Q9M7E7	arabidopsis
28	718.5	40.9	325	10	Q9LH52	Q9LH52	arabidopsis
29	699	39.8	253	10	Q9LUX1	Q9LUX1	pyrus pyrifolia
30	630	35.9	313	10	Q9XHD6	Q9XHD6	glycine max
31	575	32.7	313	10	Q9J8E5	Q9J8E5	glycine max
32	457.5	26.1	214	10	Q9LH53	Q9LH53	arabidopsis
33	439	25.0	203	10	Q9C7D9	Q9C7D9	arabidopsis
34	431.5	24.6	372	10	Q9LHR0	Q9LHR0	arabidopsis
35	411.5	23.4	478	10	Q9FWX5	Q9FWX5	arabidopsis
36	408.5	23.3	371	10	Q9LXU5	Q9LXU5	arabidopsis
37	401	22.8	480	10	Q48705	Q48705	arabidopsis
38	398.5	22.7	365	10	Q9L739	Q9L739	arabidopsis
39	398.5	22.7	512	10	Q9FW47	Q9FW47	arabidopsis
40	384	21.9	589	10	Q9FHI8	Q9FHI8	arabidopsis
41	378	21.5	976	10	Q42371	Q42371	arabidopsis
42	370	21.1	486	10	Q9L021	Q9L021	arabidopsis
43	370	21.1	907	10	Q9FW49	Q9FW49	arabidopsis
44	370	21.1	943	10	Q9SR17	Q9SR17	arabidopsis
45	363.5	20.7	1036	10	Q9FN37	Q9FN37	arabidopsis

ALIGNMENTS

RESULT 1

082438 PRELIMINARY: PRT: 332 AA

082438

01-NOV-1998 (TEMBLrel. 08, Last sequence update)

01-NOV-1998 (TEMBLrel. 08, Last sequence update)

01-JUN-2001 (TEMBLrel. 17, Last annotation update)

ANTIFREEZE PROTEIN.

AF.

Daucus carota (Carrot).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

NCBI_TaxId=4039;

SEQUENCE FROM N.A.

STRAIN-CV. AUTUMN KING; TISSUE=TAP ROOT;

MDLINE=98429644; PubMed=9756474;

RA	Morrall D., Elias L., Ashford D., Smallwood M., Sidebottom C., Lillford P., Telford J., Holt C., Bowles D.
RT	"A carrot leucine-rich repeat protein that inhibits ice recrystallization."
RL	Science 282:115-117(1998).

SEQUENCE FROM N.A.

STRAIN-CV. NEWMARKET FL;

MDLINE=99229753; PubMed=10214940;

RA	Meyer K., Keil W., Naldrett M.
RT	"A leucine-rich repeat protein of carrot that exhibits antifreeze activity."
RL	FEBS Lett. 447:171-178(1999).
DR	EMBL: AF055480; AAC62932.1; -
DR	EMBL: AJ133400; CAB37347.1; -
DR	Mendel: 33027; Dauca:2327;33027.
DR	InterPro: IPR001611; LRR.
DR	InterPro: IPR003592; LRR_out.
DR	Pfam: PF00560; LRR: 4.
DR	SMART: SM00370; LRR: 4.
KW	Signal
QO	SEQUENCE 332 AA; 36845 MW; EEEF6FAEBEAAE202 CnC64;

Query Match 100.0%; Score 1756; DB 10; Length 332;
 Best Local Similarity 100.0%; Pred. No. 9.6e-146;
 Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNIESFPCILICMIFLCPLNLSASQRCNNNDKQALLQITALKNPITDSWVSDCC 60
 DB 1 MNIESFPCILICMIFLCPLNLSASQRCNNNDKQALLQITALKNPITDSWVSDCC 60
 QY 61 GMDLVECDTSSNRITSLIIODEALGOIPPOVGDPLYQALMFRKLPNLFGKIPPEISA 120
 DB 61 GMDLVECDTSSNRITSLIIODEALGOIPPOVGDPLYQALMFRKLPNLFGKIPPEISA 120
 QY 121 LKDKSLRSLSSLSGVPPLFPFPPOLTKLCLDSFNKLLGVIPOLSTLPNLKALHLERN 180
 DB 121 LKDKSLRSLSSLSGVPPLFPFPPOLTKLCLDSFNKLLGVIPOLSTLPNLKALHLERN 180
 QY 181 ELTGEIPDIFGNFAGSPDLYLSHNLGTGFVPTFARADPIRLDFSGNRLGDISFLFGPK 240
 DB 181 ELTGEIPDIFGNFAGSPDLYLSHNLGTGFVPTFARADPIRLDFSGNRLGDISFLFGPK 240
 QY 241 KRLEMLDSSGNVLSNFESRVOEPFSLTYLDLNHOISGSLSELAKLDOTFNVSNNL 300
 DB 241 KRLEMLDSSGNVLSNFESRVOEPFSLTYLDLNHOISGSLSELAKLDOTFNVSNNL 300
 QY 301 CGKIPTGSLQRFDRATAYLHNSCLGAPLPEC 332
 DB 301 CGKIPTGSLQRFDRATAYLHNSCLGAPLPEC 332

RESULT 2
 Q38695 PRELIMINARY; PRT; 327 AA.
 AC Q38695;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE POLYGALACTURONASE INHIBITOR PRECURSOR.
 CN PCIP.
 OS Actinidia chinensis (kiwi) (Yangtao).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
 OC Asteridae: Ericales; Actinidiaceae; Actinidia.
 OX NCBI_TaxID=3625;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=HAYWARD; TISSUE=UNRIPE FRUIT;
 RC Simpson C.G., Gardier R.C.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z48063; CA88846.1;
 DR Mendel: 14029; Accch: 2327; 14029.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR Pfam: PF00560; LRR: 6.
 DR SMART: SM00370; LRR: 6.
 DR Signal.
 KW signal.
 FT CHAIN 1 21 POTENTIAL.
 FT CHAIN 22 327 POLYGALACTURONASE INHIBITOR.
 SQ SEQUENCE 327 AA; 36163 MW; 9335E02978378765 CRC64;

Query Match 53.4%; Score 937.5; DB 10; Length 327;
 Best Local Similarity 59.9%; Pred. No. 4.3e-74;
 Matches 191; Conservative 35; Mismatches 90; Indels 3; Gaps 3;

QY 15 MIFCLPLNLSASQRCNNNDKQALLQITALKNPITDSWVSDCCGMDLVECDTSSNR 74
 DB 10 LRFSLSLSPSLSDCNCNDKQALLQITALKNPITDSWVSDCCGMDLVECDTSSNR 74
 QY 75 ISLIIODEALGOIPPOVGDPLYQALMFRKLPNLFGKIPPEISALKDKLSRLSSTL 134
 DB 70 IALTIFSGN-1SGQIPAAVGDPLYQTLIFRKLNSLTGQIPSAISKLSNLMKVRSLSWNL 128
 QY 135 SGVPPLFPFPPOLTKLCLDSFNKLLGVIPOLSTLPNLKALHLERNELTGEIPDIFGNFA 194

DB 129 SGVPSPFSQALKNLTFDLDSFNDLTGSTSPSSSKLTNDAHLDRNKLGTGIPNSFGFT 188
 QY 195 GS-PDIYLSHNLGTGFVPTFARADPIRLDFSGNRLGDISFLFGPKRLEMLDFSGNVL 253
 DB 189 GQVDPDLSHNLGTGIRKTLGDLNFIVDSRNMLSGDISFMSGNKTQIDVFSRNF 248
 QY 254 SFNFSRVOEPFSLTYLDLNHOISGSLSELAKLDOTFNVSNNLCKGKIPFGNLDOR 313
 DB 249 QFDLSKV-VFQSLTSLDLSLNHKIYGSLPVGLTKLDLYLVNYSNRLCGHLPFGKLOGF 307
 QY 314 DRFAYLHNSCLGAPLPEC 332
 DB 308 DQTSYFNHRCGAPLPDC 326

RESULT 3
 Q9AXP4 PRELIMINARY; PRT; 333 AA.
 AC Q9AXP4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE POLYGALACTURONASE INHIBITING PROTEIN.
 OS Vitis vulpifera (Grape).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Vitaceae;
 OC Vitis.
 OX NCBI_TaxID=29760;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=CV. CHARCONNAY; TISSUE=LEAVES;
 RC Bezier A., Lambert B., Baillieu F.;
 RT "Molecular cloning of a grapevine gene coding for polygalacturonase
 inhibiting protein."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF305093; AK14075.1;
 SQ SEQUENCE 333 AA; 36975 MW; 57BB840E1096C4FD CRC64;

Query Match 50.9%; Score 894; DB 10; Length 333;
 Best Local Similarity 56.0%; Pred. No. 2.8e-70;
 Matches 187; Conservative 40; Mismatches 101; Indels 6; Gaps 4;

QY 3 IESSFPCILICMIFLCPLNLSASQRCNNNDKQALLQITALKNPITDSWVSDCC 59
 DB 1 METSKLFLSSLLVLLATRPCSLSRCPKDKVLLQIKKALDPPYILASNNPNTDC 60
 QY 60 CGMDLVECDTSSNRITSLIIODEALGOIPPOVGDPLYQALMFRKLPNLFGKIPPEIS 119
 DB 61 CGMWCEVCDLTHRHNSLTJFSGQ-LSGOIPDAVGDDPLETLIFRKLNSLTGQIPPAIA 119
 QY 120 ALKLSLRLSSTLSGVPPLFPFPPOLTKLCLDSFNKLLGVIPOLSTLPNLKALHLER 179
 DB 120 KLKHLKMWRLSWNLFGVPVAFSELNKLTLLDSFNNSLSPFGSLPLNLAHLIDR 179
 QY 180 NELTGEIPDIFGNFAGS-PDIYLSHNLGTGFVPTFARADPIRLDFSGNRLGDISFLFG 238
 DB 180 NHLGPIPDSPGKFASTPGHLHSHNLSGKIPYSFSGFDPNNVMDLSRNLKEGDLSTFFN 239
 QY 239 PKRLEMLDSSGNVLSNFESRVOEPFSLTYLDLNHOISGSLSELAKLDOTFNVSND 298
 DB 240 ANKSTQIVDESRLNFQFDLSRV-EFPKSLTSLDSHNKIGSLPEMNTSLDLOFLNVSYN 298
 QY 299 NLGKIPTGSLQRFDRATAYLHNSCLGAPLPEC 332
 DB 299 RLCGKIPVGGKLOSFDYDSTFHNRCGAPLPDC 332

RESULT 4
 P93270 PRELIMINARY; PRT; 330 AA.
 ID P93270;
 AC P93270;

QY 63 DLVECDSTSNRIISLIIODEALTGQIPPOVGDLPYLQALWFRKLPNLFGKIPPEISALK 122
 Db 61 YCVTGDSTNRINSLIFAGQ-VSGQIPPOVGDLPYLELFEHKKQPNLGPISIAK 119
 QY 123 DKSRLSTSGPVLPFPOLTKLCLDLSFNKLGVIPQSLTPNLKALHNERNEL 182
 Db 120 LKLELRSLWTNINSGVPPLSOLKNLFLDLFSNLTGSIPLSMQLPNNLALRVDRNKL 179
 QY 183 TGEIPDIFGNFAGS-PDIYLSHNLQTLGVFPKTFARADPIRLDFSGNRLGEGISLFGPKK 241
 Db 180 TGHIPKSGFGEVGDVPLDYLHNLQSLGTPTSLAKLNSTIDFSNNKLEGASMTFGINK 239
 QY 242 RLEMIDFSGNVLNFSNVQEPDPSLYLDLNHNOISGSLSELAKLDLQTFNVSNNMLC 301
 Db 240 TQIVDLSRNLLEINLSNV-EFSKSLTSLDLNNHKKITGIVGLQVLDQPLANSYNMLC 298
 QY 302 GKIPGGLORFDRFAYLHNSCLGAPLPEC 332
 Db 299 GQIPVGGKIQSFSDSYFHNRCICGAPLPSC 329

RESULT 7
 ID 080399 PRELIMINARY; PRT; 327 AA.
 AC 080399;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 GN POLYGALACTURONASE-INHIBITING PROTEIN.
 OS Citrus sp. cv. sannumphung.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Sapindales; Rutaceae; Citrus.
 RN NCBI_TaxID=77791;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SANNUMPHUNG;
 RA Nalumpang S., Akimitsu K., Yamamoto H.;
 RT "Polygalacturonase-inhibiting protein (PGIP) gene of citrus (cv. sannumphung)".
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB015356; BAA29024.1;
 DR Mendel; 31062; Citsp;2327;31062.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003592; LRR_out.
 DR Pfam; PF00560; LRR; 4.
 DR SMART; SM00370; LRR; 5.
 SO SEQUENCE 327 AA; 36177 MW; EA0BEDD6C0ED87A5 CRC64;

Query Match 48.5%; Score 851; DB 10; Length 327;
 Best Local Similarity 55.1%; Pred. No. 1.6e-66;
 Matches 177; Conservative 38; Mismatches 96; Indels 10; Gaps 5;

QY 11 LCICMIFLCPNLASQRCNNNDKQALQIKTALKNPITTSWSDDCGMDLVECDT 70
 Db 13 LCICL-----SPSLSDLCNPNDKVLLKFKKSLNNPYVLASWNPRTDCDWCYVCJDLT 66
 QY 71 SNRIISLIQDDEALTGQIPPOVGDLPYLQALWFRKLPNLFGKIPPEISALKDLKSLRLS 130
 Db 67 TNRINSLTIFAGD-LPGQIPPEVGDLPYLELFEHKKQPNLGPISIAKLNKLTLRIS 125
 QY 131 STLSGVPPLFPOLTKLCLDLSFNKLGVIPQSLTPNLKALHNERNELTGEIPDIF 190
 Db 126 WTINISGVPDFIRQTLNLTLELFSNNLSGTIPGSLKQIKGALHLDNRNKLTSIPSEF 185
 QY 191 GNFAGS-PDIYLSHNLQTLGVFPKTFARADPIRLDFSGNRLGEGISLFGPKKRLMDLFS 249
 Db 186 GTFGSIPLDYLHNLQSLGTPTSLAKLNSTIDFSNNKLEGASMTFGINKTQIRDIVS 245
 QY 250 GNVLSFNSRQVEPPPSLYLDLNHNOISGSLSELAKLD-LQTFNVSNNMLCGKIPVGG 308
 Db 305 KIQSFYGYTEYFHNRCICGAPL 325

Db 246 RNLLEFNLSKV-EFPQSLTNLDLNHKKITGIPAOITSLLENLGLNVSNNRLCGPIVGG 304
 QY 309 NLQRFDRFAYLHNSCLGAPL 329
 Db 305 KIQSFYGYTEYFHNRCICGAPL 325

RESULT 8
 ID 09SA22 PRELIMINARY; PRT; 327 AA.
 AC 09SA22;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 GN POLYGALACTURONASE-INHIBITING PROTEIN.
 OS Citrus sp. cv. sannumphung.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Sapindales; Rutaceae; Citrus.
 RN NCBI_TaxID=77791;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SANNUMPHUNG;
 RA Nalumpang S., Akimitsu K., Yamamoto H.;
 RT "Polygalacturonase-inhibiting protein (PGIP B) gene of citrus (cv. sannumphung)".
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB015643; BAA29056.1;
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003592; LRR_out.
 DR Pfam; PF00560; LRR; 4.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00370; LRR; 5.
 SO SEQUENCE 327 AA; 36168 MW; 86BA2C84C48A7177 CRC64;

Query Match 48.5%; Score 851; DB 10; Length 327;
 Best Local Similarity 55.1%; Pred. No. 1.6e-66;
 Matches 177; Conservative 38; Mismatches 96; Indels 10; Gaps 5;

QY 11 LCICMIFLCPNLASQRCNNNDKQALQIKTALKNPITTSWSDDCGMDLVECDT 70
 Db 13 LCICL-----SPSLSDLCNPNDKVLLKFKKSLNNPYVLASWNPRTDCDWCYVCJDLT 66
 QY 71 SNRIISLIQDDEALTGQIPPOVGDLPYLQALWFRKLPNLFGKIPPEISALKDLKSLRLS 130
 Db 67 TNRINSLTIFAGD-LPGQIPPEVGDLPYLELFEHKKQPNLGPISIAKLNKLTLRIS 125
 QY 131 STLSGVPPLFPOLTKLCLDLSFNKLGVIPQSLTPNLKALHNERNELTGEIPDIF 190
 Db 126 WTINISGVPDFIRQTLNLTLELFSNNLSGTIPGSLKQIKGALHLDNRNKLTSIPSEF 185
 QY 191 GNFAGS-PDIYLSHNLQTLGVFPKTFARADPIRLDFSGNRLGEGISLFGPKKRLMDLFS 249
 Db 186 GTFGSIPLDYLHNLQSLGTPTSLAKLNSTIDFSNNKLEGASMTFGINKTQIRDIVS 245
 QY 250 GNVLSFNSRQVEPPPSLYLDLNHNOISGSLSELAKLD-LQTFNVSNNMLCGKIPVGG 308
 Db 305 KIQSFYGYTEYFHNRCICGAPL 325

DE POLYGALACTURONASE INHIBITOR (PGIP).
GN Citrus unshiu (Satsuma orange).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=55188;
RN [1]
RP SEQUENCE FROM N.A.
RA Gotoku Y., Akimitsu K., Yamamoto H.;
RT "Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases."
DR EMBL: AB016204; AAA31841.1; -
DR Mendel: 31083; Citrus;2327;31083.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 4.
DR SMART: SM00370; LRR; 5.
SQ SEQUENCE 327 AA; 36147 MW; E15A8C7C90A19D5 CRC64;

Query Match 48.4%; Score 850; DB 10; Length 327;
Best Local Similarity 55.1%; Pred. No. 1.9e-66;
Matches 177; Conservative 38; Mismatches 96; Indels 10; Gaps 5;

11 LCICMIFCLPMLASORCANNNDKQALLQIKTALKNPITTSWSDCCGMDLYECDET 70
13 LCLCT-----SPSLSDICNPDKRVLLFKFKSLNPPVLAWSNPKTDCDCCDYCYTCDLT 66
71 SNRIISLIIDDEALTGQIPQVGDLPYLQALMFKRLPGLFGKIPPEISALDKLSRLS 130
67 TNRIISLTIFACD-LPGQIPPEVGDPYLETLMFKRLPSLTPIQIPALAKLNLTLRIS 125
131 STLSGVPVLPFPQTLTKLCTLDLSFNKLGVIPQISTLPNLKALHLERNELTGEIPDIF 190
126 WNISGVPVDFIROLTNLTFLELSFNLSGTLPGSLSKLOKLGALHLDRNKLTSIPESF 185
191 GNFAGS-PDIYLSHQNLGTFVPKTFARADPIRLDPSGNRLEEDISFLGPKRRLMDFS 249
186 GFTGTSIDPLYLSHQNLGSKIPASLSGMDENTIDLSRNKLEGDASFGLNKTTRIDVS 245
250 GNVLSFNFSRVOEPPPSLTLYLDLNHNQISLSSELAELD-LQTFNVSNNLCGKIPITG 308
246 RNLLEFNLSKV-EFPOSLTNLDLNHNKIFGSIPTQITSLNGLFNLSVNRCLGPIPVGG 304
309 NLQRFRTAYLHNSCLCGAPL 329
305 KLSFGYTEYEFHNRCLCGAPL 325

RESULT 10
096401 PRELIMINARY; PRT: 327 AA.
AC 096401:
DT 01-FEB-1997 (TREMblrel. 02. Created)
DT 01-FEB-1997 (TREMblrel. 02. Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17. Last annotation update)
DE POLYGALACTURONASE-INHIBITING PROTEIN.
OS Citrus sinensis (Sweet orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=2711;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAWLIN; TISSUE=CALLUS;
RA Mayer R.T.;
RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: Y08618; CAA6910.1; -
DR Mendel: 14033; Citri;2327;14033.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00560; LRR; 4.

DR SMART: SM00370; LRR; 5.
SQ SEQUENCE 327 AA; 36216 MW; 151F5C7C8BBA8D5 CRC64;

Query Match 48.3%; Score 849; DB 10; Length 327;
Best Local Similarity 55.1%; Pred. No. 2.4e-66;
Matches 177; Conservative 38; Mismatches 96; Indels 10; Gaps 5;

11 LCICMIFCLPMLASORCANNNDKQALLQIKTALKNPITTSWSDCCGMDLYECDET 70
13 LCLCT-----SPSLSDICNPDKRVLLFKFKSLNPPVLAWSNPKTDCDCCDYCYTCDLT 66
71 SNRIISLIIDDEALTGQIPQVGDLPYLQALMFKRLPGLFGKIPPEISALDKLSRLS 130
67 TNRIISLTIFACD-LPGQIPPEVGDPYLETLMFKRLPSLTPIQIPALAKLNLTLRIS 125
131 STLSGVPVLPFPQTLTKLCTLDLSFNKLGVIPQISTLPNLKALHLERNELTGEIPDIF 190
126 WNISGVPVDFIROLTNLTFLELSFNLSGTLPGSLSKLOKLGALHLDRNKLTSIPESF 185
191 GNFAGS-PDIYLSHQNLGTFVPKTFARADPIRLDPSGNRLEEDISFLGPKRRLMDFS 249
186 GFTGTSIDPLYLSHQNLGSKIPASLSGMDENTIDLSRNKLEGDASFGLNKTTRIDVS 245
250 GNVLSFNFSRVOEPPPSLTLYLDLNHNQISLSSELAELD-LQTFNVSNNLCGKIPITG 308
246 RNLLEFNLSKV-EFPOSLTNLDLNHNKIFGSIPTQITSLNGLFNLSVNRCLGPIPVGG 304
309 NLQRFRTAYLHNSCLCGAPL 329
305 KLSFGYTEYEFHNRCLCGAPL 325

RESULT 11
040160 PRELIMINARY; PRT: 327 AA.
AC 040160:
DT 01-NOV-1996 (TREMblrel. 01. Created)
DT 01-NOV-1996 (TREMblrel. 01. Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17. Last annotation update)
DE POLYGALACTURONASE INHIBITOR PROTEIN PRECURSOR.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VENT. CHERRY;
RX MEDLINE=94339475; PubMed=8061315;
RA Stoltz H.U., Contos J.J., Powell A.L., Bennett A.B., Labavitch J.M.;
RT "Structure and expression of an inhibitor of fungal polygalacturonases from tomato."
RL Plant Mol. Biol. 25: 607-617 (1994).
DR EMBL: L26529; AAA53547.1; -
DR Mendel: 14032; Lycos;2327;14032.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00560; LRR; 5.
DR SMART: SM00370; LRR; 4.
KW signal.
FT SIGNAL. 1 20 POTENTIAL.
FT CHAIN 21 327 POLYGALACTURONASE INHIBITOR PROTEIN.
SQ SEQUENCE 327 AA; 36490 MW; DCD61BF647D03FAL CRC64;

Query Match 48.1%; Score 844; DB 10; Length 327;
Best Local Similarity 52.8%; Pred. No. 6.5e-66;
Matches 171; Conservative 46; Mismatches 103; Indels 4; Gaps 3;

11 LCICMIFCLPMLASORCANNNDKQALLQIKTALKNPITTSWSDCCGMDLYECDET 70
5 LLLVYIFLCFASPSLSVRCNPKDKRVLLQIKKDLGNPFLHLSMDPNTDCCYWIYVICKDR 64

